

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wild, Martha A.
Cochran, Mark D.
- (ii) TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 72
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Cooper & Dunham LLP
 - (B) STREET: 1185 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 23-MAR-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/126,597
 - (B) FILING DATE: 24-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: White, John P.
 - (B) REGISTRATION NUMBER: 28,678
 - (C) REFERENCE/DOCKET NUMBER: 39116-A
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 278-0400
 - (B) TELEFAX: (212) 391-0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1059..2489
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2575..4107

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- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 4113..4445
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 4609..5487
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 5697..8654
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 9874..10962
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 11159..12658
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 12665..13447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCGTGC CCC TAAAGGCCGC CGAGAAAGCT AAGTCCAAAT GTGACGTCGG AGGTCTCGAC	60
ATGGTCGCCA ACCCTCCAAA TGCTACCCGC CGGCCACGC AACGCGGGCT TTTATAAGA	120
TGGCGCGCGA GACAATAACA CTTACTCATC CGCGTACGGC TTTATTATTG TCAATATTTG	180
TGTGTTATT ATTACTGCTA CGGCCCTTGT TTCTGCAAGG CCCTCGCCGC GGCCAGGCC	240
ACTATTCCGG CAGCGGCCGC CGACGCGGCG AGCGTCGCGC CTAACGTCGG CGCCGCGGGG	300
AGCGGGGTTT CTTCGACTTA AATAGACTCC CGAGAAAAAA TTTTGGCTGC CGTTCGCCAT	360
CATCCGAGTC GGAACACAG TATGCGGCCG AGTTAGGTTT TACTTTTAAA AACTTTACCG	420
TGCTGTACGG CCAGGGCGTT CTCAGGCTCG AAGGGGCAAG AGTTGTCCAG ACTGATGGGT	480
GACTCAGAGA CAGCGTTGTC TTGTCTCGGT TTACCAAAAA TATTCCACT CCTCTCTCAA	540
AATTTTACC TCCGGTTTCG GTAATTAGGA AAGTTTTTGG CGCAGGGAGG TTTAAAGCTG	600
CCATGCATAT GTCAGCGGTA CCCAGCACCC ACAAATGGAA CTCTTTTGGC GCATACGCGC	660
CAGATGACAA ATGTTAAAC CCTGCGTCCA AGCCGCTCCA CTCGGGACTT ACTCCAGGCG	720
GGTCGCCCC CTCACCGAAC CGAATCACGG GTCTGCACAT CCTGGGAAGG GAAACAGCT	780
CCCCGAAAC TTCTACAGA GATGCCGGGC GCACGATTAC CGATAATGTA CTCGGACGAT	840
CGTAACTCGC CATAGTTTTC ACTGCGTGAA CCAATCTTTT CCATCCAGAA TCCGAGAGCT	900
CAAACTAGA ATTAGTAGT TTGTAGTGGC AATCGACCGC AGAAACTATA GTCACTTTTA	960
CAGGCGCCAT CGCCGCTCAG ACTCCACCCC GCTATGATGT CAGAAATATA ACGCTCTTAT	1020
TCTAGCAGAG TCAGGCCAAT ATATACAGCT TAGAGAAG ATG CGG TTT CGG CGC	1073
Met Arg Phe Arg Arg	
1 5	
ATC TGT TCA CGC TCT AGG GCA GAA AAA CGA AGA AGA ACA ACC GAG AAT	1121
Ile Cys Ser Arg Ser Arg Ala Glu Lys Arg Arg Arg Thr Thr Glu Asn	
10 15 20	

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CCG CTT ACC TCA AAA CGC GTT TGC GTA TTG GAT AGT TTC TCA CGG ACA Pro Leu Thr Ser Lys Arg Val Cys Val Leu Asp Ser Phe Ser Arg Thr 25 30 35	1169
ATG TCA TTG CGC CCC TAT GCA GAA ATT TTG CCG ACC GCG GAA GGC GTC Met Ser Leu Arg Pro Tyr Ala Glu Ile Leu Pro Thr Ala Glu Gly Val 40 45 50	1217
GAG CGC CTC GCC GAA CTT GTT AGT GTG ACA ATG ACA GAA CGC GCG GAA Glu Arg Leu Ala Glu Leu Val Ser Val Thr Met Thr Glu Arg Ala Glu 55 60 65	1265
CCT GTG ACA GAG AAT ACA GCT GTA AAC AGT ATC CCC CCG GCT AAC GAG Pro Val Thr Glu Asn Thr Ala Val Asn Ser Ile Pro Pro Ala Asn Glu 70 75 80 85	1313
AAC GGG CAG AAC TTC GCA TAT GCA GGC GAT GGG CCC TCG ACT ACT GAA Asn Gly Gln Asn Phe Ala Tyr Ala Gly Asp Gly Pro Ser Thr Thr Glu 90 95 100	1361
AAA GTT GAC GGC TCG CAT ACA GAC TTC GAT GAA GCA TCG AGC GAC TAC Lys Val Asp Gly Ser His Thr Asp Phe Asp Glu Ala Ser Ser Asp Tyr 105 110 115	1409
GCC GGC CCT GTC CCG CTC GCG CAA ACT AGA TTG AAG CAT TCG GAT GAA Ala Gly Pro Val Pro Leu Ala Gln Thr Arg Leu Lys His Ser Asp Glu 120 125 130	1457
TTT CTT CAG CAC TTC CGA GTT TTA GAC GAT TTG GTG GAG GGG GCT TAC Phe Leu Gln His Phe Arg Val Leu Asp Asp Leu Val Glu Gly Ala Tyr 135 140 145	1505
GGG TTT ATC TGC GGC GTC CGT CGC TAC ACC GAG GAA GAG CAA CGT CGA Gly Phe Ile Cys Gly Val Arg Arg Tyr Thr Thr Glu Glu Gln Arg Arg 150 155 160 165	1553
AGA GGG GTT AAC AGT ACT AAC CAG GGG AAA TCA AAA TGT AAG CGC CTG Arg Gly Val Asn Ser Thr Asn Gln Gly Lys Ser Lys Cys Lys Asp Leu 170 175 180	1601
ATA GCT AAA TAT GTG AAA AAT GGA ACA AGG GCG GCC TCT CAG CTG GAA Ile Ala Lys Tyr Val Lys Asn Gly Thr Arg Ala Ala Ser Gln Leu Glu 185 190 195	1649
AAT GAA ATT TTG GTT CTC GGG CGC CTA AAT CAC GAG AAT GTT CTC AAG Asn Glu Ile Leu Val Leu Gly Arg Leu Asn His Glu Asn Val Leu Lys 200 205 210	1697
ATC CAG GAA ATC CTT CGG TAC CCG GAT AAT ACG TAC ATG TTA ACG CAG Ile Gln Glu Ile Leu Arg Tyr Pro Asp Asn Thr Tyr Met Leu Thr Gln 215 220 225	1745
AGG TAT CAG TTC GAC TTG TAC AGC TAC ATG TAC GAT GAA GCG TTC GAC Arg Tyr Gln Phe Asp Leu Tyr Ser Tyr Met Tyr Asp Glu Ala Phe Asp 230 235 240 245	1793
TGG AAA GAC AGT CCA ATG CTT AAA CAG ACT AGA CGC ATC ATG AAG CAG Trp Lys Asp Ser Pro Met Leu Lys Gln Thr Arg Arg Ile Met Lys Gln 250 255 260	1841
CTC ATG TCA GCG GTC TCG TAT ATC CAT TCA AAG AAA CTG ATT CAC AGG Leu Met Ser Ala Val Ser Tyr Ile His Ser Lys Lys Leu Ile His Arg 265 270 275	1889
GAC ATC AAA CTC GAA AAT ATT TTC TTA AAC TGC GAC GGC AAG ACA GTG Asp Ile Lys Leu Glu Asn Ile Phe Leu Asn Cys Asp Gly Lys Thr Val 280 285 290	1937

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CTG GGC GAC TTT GGA ACT GTC ACG CCT TTT GAA AAT GAG CGG GAG CCC Leu Gly Asp Phe Gly Thr Val Thr Pro Phe Glu Asn Glu Arg Glu Pro 295 300 305	1985
TTT GAA TAT GGA TGG GTG GGG ACC GTG GCT ACT AAC TCT CCC GAG ATA Phe Glu Tyr Gly Trp Val Gly Thr Val Ala Thr Asn Ser Pro Glu Ile 310 315 320 325	2033
CTC GCC AGG GAT TCG TAC TGT GAA ATT ACA GAC ATT TGG AGC TGC GGA Leu Ala Arg Asp Ser Tyr Cys Glu Ile Thr Asp Ile Trp Ser Cys Gly 330 335 340	2081
GTA GTA TTG CTG GAA ATG GTA AGC CAT GAA TTT TGC CCG ATC GGC GAT Val Val Leu Leu Glu Met Val Ser His Glu Phe Cys Pro Ile Gly Asp 345 350 355	2129
GGC GGG GGA AAT CCG CAC CAG CAA TTG CTG AAA GTT ATC GAC TCT CTC Gly Gly Gly Asn Pro His Gln Leu Leu Lys Val Ile Asp Ser Leu 360 365 370	2177
TCA GTT TGT GAT GAA GAG TTC CCA GAC CCC CCG TGT AAT CTG TAC AAT Ser Val Cys Asp Glu Glu Phe Pro Asp Pro Cys Asn Leu Tyr Asn 375 380 385	2225
TAT TTG CAT TAT GCG AGC ATC GAT CGC GCC GGA CAT ACG GTC CCG TCG Tyr Leu His Tyr Ala Ser Ile Asp Arg Ala Gly His Thr Val Pro Ser 390 395 400 405	2273
CTC ATA CGG AAC CTC CAC CTT CCG GCG GAT GTG GAA TAC CCT CTA GTT Leu Ile Arg Asn Leu His Leu Pro Ala Asp Val Glu Tyr Pro Leu Val 410 415 420	2321
AAA ATG CTT ACT TTT GAC TGG CGT TTG AGA CCC AGC GCG GCC GAA GTA Lys Met Leu Thr Phe Asp Trp Arg Leu Arg Pro Ser Ala Ala Glu Val 425 430 435	2369
TTG GCA ATG CCA CTG TTT TCG GCT GAA GAG GAA CGG ACC ATA ACA ATT Leu Ala Met Pro Leu Phe Ser Ala Glu Glu Thr Arg Thr Ile Thr Ile 440 445 450	2417
ATT CAT GGA AAA CAT AAA CCC ATC CGA CCC GAA ATC CGT GCG CGG GTG Ile His Gly Lys His Lys Pro Ile Arg Pro Glu Ile Arg Ala Arg Val 455 460 465	2465
CCA CGG TCC ATG AGT GAA GGT TAATAATAAA GGACGGAGAT AGAGAACTGA Pro Arg Ser Met Ser Glu Gly 470 475	2516
AGCGTCAGAT TTTTITAAAA AAATAAATGA TCGAGAAGCTT ATGATTGTCT TTTCTTGA	2574
ATG ACC TTG CCC CAT CGA TTA ACG AAA AGA CCT TTC GCG CGT CGA TTC Met Thr Leu Pro His Arg Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe 1 5 10 15	2622
TGC TCG GTC TTT GTG ATA CAT TAT AGT GAG ACT AAA CTC GAC CGA TAT Cys Ser Val Phe Val Ile His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr 20 25 30	2670
AAC AAG ACA ATG TTA CTC TAT AGA CCG GAC TCA ACC ATG CGG CAT AGC Asn Lys Thr Met Leu Leu Tyr Arg Pro Asp Ser Thr Met Arg His Ser 35 40 45	2718
GGA GGC GAC GCA AAT CAC AGA GGG ATA AGG CCG AGG CGG AAA TCT ATT Gly Gly Asp Ala Asn His Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile 50 55 60	2766

GGA GCG TTT AGC GCG CGC GAA AAG ACT GGA AAA CGA AAT GCG CTG ACG Gly Ala Phe Ser Ala Arg Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr 65 70 75 80	2814
GAA AGC AGC TCC TCC TCC GAC ATG CTA GAT CCG TTT TCC ACG GAT AAG Glu Ser Ser Ser Ser Asp Met Leu Asp Pro Phe Ser Thr Asp Lys 85 90 95	2862
GAA TTT GGC GGT AAG TGG ACG GTA GAC GGA CCT GCC GAC ATT ACT GCC Glu Phe Gly Gly Lys Trp Thr Val Asp Gly Pro Ala Asp Ile Thr Ala 100 105 110	2910
GAG GTC CTT TCT CAG GCA TGG GAC GTT CTC CAA TTA GTG AAG CAT GAA Glu Val Leu Ser Gln Ala Trp Asp Val Leu Gln Leu Val Lys His Glu 115 120 125	2958
GAT GCG GAG GAG GAG AGA GTG ACT TAT GAG TCC AAA CCG ACC CCG ATA Asp Ala Glu Glu Glu Arg Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile 130 135 140	3006
CAG CCG TTC AAT GCC TGG CCG GAC GGG CCG AGT TGG AAC GCG CAG GAT Gln Pro Phe Asn Ala Trp Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp 145 150 155 160	3054
TTT ACT CGA GCG CCA ATA GTT TAT CCC TCT GCG GAG GTA TTG GAC GCA Phe Thr Arg Ala Pro Ile Val Tyr Thr Ser Ala Glu Val Leu Asp Ala 165 170 175	3102
GAG GCG TTG AAA GTA GGG GCA TTC GTT AGC CGA GTT TTA CAA TGT GTA Glu Ala Leu Lys Val Gly Ala Phe Val Ser Arg Val Leu Gln Cys Val 180 185 190	3150
CCG TTC ACG CGA TCA AAG AAA AGC GTT ACG GTG CCG GAT GCG CAG TCG Pro Phe Thr Arg Ser Lys Lys Ser Val Thr Val Asp Ala Gln Ser 195 200 205	3198
TTT TTG GGG GAC TCG TTC TGG AGA ATA ATG CAG AAC GTT TAC ACG GTT Phe Leu Gly Asp Ser Phe Trp Arg Ile Met Gln Asn Val Tyr Thr Val 210 215 220	3246
TGC TTA CGA CAG CAC ATA ACT CGA CTC AGG CAC CCT TCC AGC AAA AGC Cys Leu Arg Gln His Ile Thr Arg Leu Arg His Pro Ser Ser Lys Ser 225 230 235 240	3294
ATT GTT AAC TGC AAC GAC CCT CTA TGG TAC GCC TAC GCG AAT CAA TTT Ile Val Asn Cys Asn Asp Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe 245 250 255	3342
CAC TGG AGA GGA ATG CGC GTG CCG TCG CTT AAA TTA GCC TCT CCC CCG His Trp Arg Gly Met Arg Val Pro Ser Leu Lys Leu Ala Ser Pro Pro 260 265 270	3390
GAG GAG AAT ATT CAA CAC GGC CCA ATG GCC GCC GTT TTT AGA AAC GCG Glu Glu Asn Ile Gln His Gly Pro Met Ala Ala Val Phe Arg Asn Ala 275 280 285	3438
GGG GCT GGT CTG TTC CTG TGG CCT GCC ATG CGC GCA GCC TTT GAA GAG Gly Ala Gly Leu Phe Leu Trp Pro Ala Met Arg Ala Ala Phe Glu Glu 290 295 300	3486
CGC GAC AAG CGA CTG TTA AGA GCA TGC CTG TCT TCA CTC GAT ATC ATG Arg Asp Lys Arg Leu Leu Arg Ala Cys Leu Ser Ser Leu Asp Ile Met 305 310 315 320	3534
GAC GCA GCC GTC CTC GCG TCG TTT CCA TTT TAC TGG CGC GGC GTC CAA Asp Ala Ala Val Leu Ala Ser Phe Pro Phe Tyr Trp Arg Gly Val Gln 325 330 335	3582

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GAC ACC TCG CGC TTC GAG CCT GCG CTG GGC TGT TTG TCA GAG TAC TTT Asp Thr Ser Arg Phe Glu Pro Ala Leu Gly Cys Leu Ser Glu Tyr Phe 340 345 350	3630
GCA CTA GTG GTG TTA CTG GCC GAG ACG GTC TTA GCG ACC ATG TTC GAC Ala Leu Val Val Leu Leu Ala Glu Thr Val Leu Ala Thr Met Phe Asp 355 360 365	3678
CAC GCA CTG GTA TTC ATG AGG GCG CTG GCA GAC GGC AAT TTC GAT GAC His Ala Leu Val Phe Met Arg Ala Leu Ala Asp Gly Asn Phe Asp Asp 370 375 380	3726
TAT GAC GAA ACT AGA TAT ATA GAC CCC GTT AAA AAC GAG TAC CTG AAC Tyr Asp Glu Thr Arg Tyr Ile Asp Pro Val Lys Asn Glu Tyr Leu Asn 385 390 395 400	3774
GGA GCC GAG GGT ACT CTG TTA CGG GGC ATA GTG GCC TCC AAC ACC GGT Gly Ala Glu Gly Thr Leu Leu Arg Gly Ile Val Ala Ser Asn Thr Ala 405 410 415	3822
CTG GCG GTG GTT TGC GCA AAC ACC TAT TCG ACG ATA AGA AAA CTC CCG Leu Ala Val Val Cys Ala Asn Thr Tyr Ser Thr Ile Arg Lys Leu Pro 420 425 430	3870
TCC GTG GCA ACT AGC GCG TGC AAT GTT GCC TAC AGG ACC GAA ACG CTG Ser Val Ala Thr Ser Ala Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu 435 440 445	3918
AAA GCG AGG CGC CCT GGC ATG AGC GAC ATA TAC CGG ATA TTA CAA AAA Lys Ala Arg Arg Pro Gly Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys 450 455 460	3966
GAG TTT TTC TTT TAC ATT GCG TGG CTC CAG AGG GTT GCA ACA CAC GCA Glu Phe Phe Phe Thr Ile Ala Trp Leu Gln Arg Val Ala Thr His Ala 465 470 475 480	4014
AAT TTC TGT TTA AAC ATT CTG AAG AGA AGC GTG GAT ACG GGC CCC CGC Asn Phe Cys Leu Asn Ile Leu Lys Arg Ser Val Asp Thr Gly Pro Arg 485 490 495	4062
CAT TTT TGT TCA GGG CCA GCT CGG AGA AGC GGC TGC AGC AGT TAAATAAA His Phe Cys Ser Gly Pro Ala Arg Arg Ser Gly Cys Ser Ser 500 505 510	4112
ATG CTC TGC CCC CTT CTC GTG CCG ATT CAA TAT GAA GAC TTT TCG AAG Met Leu Cys Pro Leu Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser Lys 1 5 10 15	4160
GCC ATG GGG TCT GAG CTC AAG AGG GAA AAG TTA GAG ACA TTC GTT AAA Ala Met Gly Ser Glu Leu Lys Arg Glu Lys Leu Glu Thr Phe Val Lys 20 25 30	4208
GCT ATT TCC AGC GAC AGG GAC CCG AGG GGG TCC TTA AGA TTT CTC ATT Ala Ile Ser Ser Asp Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu Ile 35 40 45	4256
TCG GAC CAT GCA AGG GAA ATT ATT GCA GAC GGA GTA CGG TTT AAG CCG Ser Asp His Ala Arg Glu Ile Ile Ala Asp Gly Val Arg Phe Lys Pro 50 55 60	4304
GTG ATA GAC GAG CCG GTT CGG GCT TCA GTT GCG CTG AGT ACC GCT GCC Val Ile Asp Glu Pro Val Arg Ala Ser Val Ala Leu Ser Thr Ala Ala 65 70 75 80	4352
GCT GGG AAA GTG AAA GCG CGA CGC TTA ACC TCA GTT CGC GCG CCC GTA Ala Gly Lys Val Lys Ala Arg Arg Leu Thr Ser Val Arg Ala Pro Val 85 90 95	4400

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CCG CCC GCA GGC GCC GTT TCC GCG CGG AAA TCG GAA ATA TGA TA	4447
Pro Pro Ala Gly Ala Val Ser Ala Arg Lys Ser Glu Ile *	
100 105 110	
AAAATGCTTG GCATTTGCGG GCGAAGAGGC GTGATCTGAA GGGCTCCACA ATGACGTAAC	4507
TGAGCTACGC ATCCCTATAA AGTGTACSCG CTGACCGCTA GCCCATACAG TGTACAGGA	4567
GGGAGAGAGAC ACAACTTCAG CTCGAAGTCT GAAGAGACAT C ATG AGC GGC	4617
Met Ser Gly	
1	
TTC AGT AAC ATA GGA TCG ATT GCC ACC GTT TCC CTA GTA TGC TCG CTT	4665
Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val Cys Ser Leu	
5 10 15	
TTG TGC GCA TCT GTA TTA GGG GCG CCG GTA CTG GAC GGG CTC GAG TCG	4713
Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly Leu Glu Ser	
20 25 30 35	
AGC CCT TTC CCG TTC GGG GGC AAA ATT ATA GCC CAG GCG TGC AAC CGC	4761
Ser Pro Phe Pro Phe Gly Gly Lys Ile Ala Gln Ala Cys Asn Arg	
40 45 50	
ACC ACG ATT GAG GTG ACG GTC CCG TGG AGC GAC TAC TCT GGT CGC ACC	4809
Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser Gly Arg Thr	
55 60 65	
GAA GGA GTG TCA GTC GAG GTG AAA TGG TTC TAC GGG AAT AGT AAT CCC	4857
Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn Ser Asn Pro	
70 75 80	
GAA AGC TTC GTG TTC GGG GTG GAT AGC GAA ACG GGC AGT GGA CAC GAG	4905
Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser Gly His Glu	
85 90 95	
GAC CTG TCT ACG TGC TGG GCT CTA ATC CAT AAT CTG AAC GCG TCT GTG	4953
Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn Ala Ser Val	
100 105 110 115	
TGC AGG GCG TCT GAC GCC GGG ATA CCT GAT TTC GAC AAG CAG TGC GAA	5001
Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys Gln Cys Glu	
120 125 130	
AAA GTG CAG AGA AGA CTG CGC TCC GGG GTG GAA CTT GGT AGT TAC GTG	5049
Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly Ser Tyr Val	
135 140 145	
TCT GGC AAT GGA TCC CTG GTG CTG TAC CCA GGG ATG TAC GAT GCC GGC	5097
Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr Asp Ala Gly	
150 155 160	
ATC TAC GCC TAC CAG CTC TCA GTG GGT GGG AAG GGA TAT ACC GGG TCT	5145
Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr Thr Gly Ser	
165 170 175	
GTT TAT CTA GAC GTC GGA CCA AAC CCC GGA TGC CAC GAC CAG TAT GGG	5193
Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp Gln Tyr Gly	
180 185 190 195	
TAC ACC TAT TAC AGC CTG GCC GAC GAG GCG TCA GAC TTA TCA TCT TAT	5241
Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu Ser Ser Tyr	
200 205 210	
GAC GTA GCC TCG CCC GAA CTC GAC GGT CCT ATG GAG GAA GAT TAT TCC	5289
Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu Asp Tyr Ser	
215 220 225	

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AAT TGT CTA GAC ATG CCC CCG CTA CGC CCA TGG ACA ACC GTT TGT TCG Asn Cys Leu Asp Met Pro Pro Leu Arg Pro Trp Thr Thr Val Cys Ser 230 235 240	5337
CAT GAC GTC GAG GAG CAG GAA AAC GCC ACG GAC GAG CTT TAC CTA TGG His Asp Val Glu Glu Gln Glu Asn Ala Thr Asp Glu Leu Tyr Leu Trp 245 250 255	5385
GAC GAG GAA TGC GCC GGT CCG CTG GAC GAG TAC GTC GAC GAA AGG TCA Asp Glu Glu Cys Ala Gly Pro Leu Asp Glu Tyr Val Asp Glu Arg Ser 260 265 270 275	5433
GAG ACG ATG CCC AGG ATG GTT GTC TTT TCA CCG CCC TCT ACG CTC CAG Glu Thr Met Pro Arg Met Val Val Phe Ser Pro Pro Ser Thr Leu Gln 280 285 290	5481
CAG TAGCCACCCG AGAGTGT TTTT TGTGAGCGC CCACGCAACA TACCTAACTG Gln	5534
CTTCATTCTT GATCAATTAT TGCATTATTGA ATAAATAAAC AGTACAAAAG CATCAGGTGT	5594
GGTTTGCGTG TCTGTGCTAA ACCATGGCGT GTGCGGGTGA AACCGTAAAT TACGTGATAA	5654
TAAATAGCAT AGGAGTTGGC GTGCAGCGTA TTTGCGCGAG AG ATG GGG ACA ATG Met Gly Thr Met 1	5708
TTA GTG TTG CGC CTT TTC CTA CTT GCA GTA GCG GAC GCG GCG TTG CCG Leu Val Leu Arg Leu Phe Leu Leu Ala Val Ala Asp Ala Ala Leu Pro 5 10 15 20	5756
ACC GGC AGA TTC TGC CGA GTT TGG AAG GTG CCT CCG GGA GGA ACC ATC Thr Gly Arg Phe Cys Arg Val Trp Lys Val Pro Gly Gly Thr Ile 25 30 35	5804
CAA GAG AAC CTG GCG GTG CTC GCG GAA TCG GCG GTC ACG GGA CAC GCG Gln Glu Asn Leu Ala Val Leu Ala Glu Ser Pro Val Thr Gly His Ala 40 45 50	5852
ACA TAT CCG CCG CCT GAA GGC GCC GTC AGC TTT CAG ATT TTT GCG GAC Thr Tyr Pro Pro Pro Glu Gly Ala Val Ser Phe Gln Ile Phe Ala Asp 55 60 65	5900
ACC CCT ACT TTG CGC ATT CGC TAC GGG CCT ACG GAG GAC GAA CTT GCA Thr Pro Thr Leu Arg Ile Arg Tyr Gly Pro Thr Glu Asp Glu Leu Ala 70 75 80	5948
CTG GAG CGC GGG ACG TCC GCC TCA GAC GCG GAC AAC GTG ACA TTT TCG Leu Glu Arg Gly Thr Ser Ala Ser Asp Ala Asp Asn Val Thr Phe Ser 85 90 95 100	5996
CTG TCA TAT CGC CCG CGC CCA GAA ATT CAC GGA GCA TAC TTC ACC ATA Leu Ser Tyr Arg Pro Arg Pro Glu Ile His Gly Ala Tyr Phe Thr Ile 105 110 115	6044
GGG GTA TTC GCT ACT GGC CAG AGC ACG GAA AGC AGC TAT TCG GTC ATC Gly Val Phe Ala Thr Gly Gln Ser Thr Glu Ser Ser Tyr Ser Val Ile 120 125 130	6092
AGT CGG GTC TTA GTT AAC GCC TCT CTG GAA CGG TCC GTG CGC CTG GAA Ser Arg Val Leu Val Asn Ala Ser Leu Glu Arg Ser Val Arg Leu Glu 135 140 145	6140
ACG CCG TGC GAT GAA AAT TTT TTG CAG AAC GAG CCT ACA TGG GGC TCG Thr Pro Cys Asp Glu Asn Phe Leu Gln Asn Glu Pro Thr Trp Gly Ser 150 155 160	6188

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AAG CGT TGG TTA GGC CCC CCG TCG CCT TAT GTG CGA GAT AAC GAT GTC Lys Arg Trp Leu Gly Pro Pro Ser Pro Tyr Val Arg Asp Asn Asp Val 165 170 175	6236
GCC GTG TTG ACA AAA GCG CAG TAC ATT GGG GAG TGC TAC TCC AAC TCG Ala Val Leu Thr Lys Ala Gln Tyr Ile Gly Glu Cys Tyr Ser Asn Ser 185 190 195	6284
GCG GCC CAG ACG GGG CTC ACG TCT CTC AAC ATG ACC TTT TTC TAT TCG Ala Ala Gln Thr Gly Leu Thr Ser Leu Asn Met Thr Phe Phe Tyr Ser 200 205 210	6332
CCT AAA AGA ATA GTA AAC GTC ACG TGG ACA ACC GGC GGC CCC TCC CCC Pro Lys Arg Ile Val Asn Val Thr Trp Thr Thr Gly Gly Pro Ser Pro 215 220 225	6380
TCG CGC ATA ACG GTA TAC TCG TCG CGG GAG AAC GGG CAG CCC GTG TTG Ser Arg Ile Thr Val Tyr Ser Ser Arg Glu Asn Gly Gln Pro Val Leu 230 235 240	6428
AGG AAC GTT TCT GAC GGG TTC TTG GTT AAG TAC ACT CCC GAC ATT GAC Arg Asn Val Ser Asp Gly Phe Leu Val Lys Tyr Thr Pro Asp Ile Asp 245 250 255 260	6476
GGC CGG GCC ATG ATA AAC GTT ATT GCC AAT TAT TCG CCG GCG GAC TCC Gly Arg Ala Met Ile Asn Val Ile Ala Asn Tyr Ser Pro Ala Asp Ser 265 270 275	6524
GGC AGC GTC CTC GCG TTT ACG GCC TTT AGG GAA GGA AAA CTC CCA TCC Gly Ser Val Leu Ala Phe Thr Ala Phe Arg Glu Gly Lys Leu Pro Ser 280 285 290	6572
GCG ATT CAA CTG CAC CGG ATA GAT ATG TCC GGG ACT GAG CCG CCG GGG Ala Ile Gln Leu His Arg Ile Asp Met Ser Gly Thr Glu Pro Pro Gly 295 300 305	6620
ACT GAA ACG ACC TTC GAC TGT CAA AAA ATG ATA GAA ACC CCG TAC CGA Thr Glu Thr Thr Phe Asp Cys Gln Lys Met Ile Glu Thr Pro Tyr Arg 310 315 320	6668
GCG CTC GGG AGC AAT GTT CCC AGG GAC GAC TCT ATC CGT CCG GGG GCC Ala Leu Gly Ser Asn Val Pro Arg Asp Asp Ser Ile Arg Pro Gly Ala 325 330 335 340	6716
ACT CTG CCT CCG TTC GAT ACC GCA GCA CCT GAT TTC GAT ACA GGT ACT Thr Leu Pro Pro Phe Asp Thr Ala Ala Pro Asp Phe Asp Thr Gly Thr 345 350 355	6764
TCC CCG ACC CCC ACT ACC GTG CCA GAG CCA GCC ATT ACT ACA CTC ATA Ser Pro Thr Thr Thr Val Pro Glu Pro Ala Ile Thr Thr Leu Ile 360 365 370	6812
CCG CGC AGC ACT AGC GAT ATG GGA TTC TTC TCC ACG GCA CGT GCT ACC Pro Arg Ser Thr Ser Asp Met Gly Phe Phe Ser Thr Ala Arg Ala Thr 375 380 385	6860
GGA TCA GAA ACT CTT TCG GTA CCC GTC CAG GAA ACG GAT AGA ACT CTT Gly Ser Glu Thr Leu Ser Val Pro Val Gln Glu Thr Asp Arg Thr Leu 390 395 400	6908
TCG ACA ACT CCT CTT ACC CTT CCA CTG ACT CCC GGT GAG TCA GAA AAT Ser Thr Thr Pro Leu Thr Leu Pro Leu Thr Thr Gly Glu Ser Glu Asn 405 410 415 420	6956
ACA CTG TTT CCT ACG ACC GCG CCG GGG ATT TCT ACC GAG ACC CCG AGC Thr Leu Phe Pro Thr Thr Ala Pro Gly Ile Ser Thr Glu Thr Pro Ser 425 430 435	7004

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GCG GCA CAT GAA ACT ACA CAG ACC CAG AGT GCA GAA ACG GTG GTC TTT Ala Ala His Glu Thr Thr Gln Thr Gln Ser Ala Glu Thr Val Val Phe 440 445 450	7052
ACT CAG AGT CCG AGT ACC GAG TCG GAA ACC GCG CGG TCC CAG AGT CAG Thr Gln Ser Pro Ser Thr Glu Ser Glu Thr Ala Arg Ser Gln Ser Gln 455 460 465	7100
GAA CCG TGG TAT TTT ACT CAG ACT CCG AGT ACT GAA CAG GCG GCT CTT Glu Pro Trp Tyr Phe Thr Gln Thr Pro Ser Thr Glu Gln Ala Ala Leu 470 475 480	7148
ACT CAG ACG CAG ATC GCA GAA ACG GAG GCG TTG TTT ACT CAG ACT CCG Thr Gln Thr Gln Ile Ala Glu Thr Glu Ala Leu Phe Thr Gln Thr Pro 485 490 495 500	7196
AGT GCT GAA CAG ATG ACT TTT ACT CAG ACT CCG GGT GCA GAA ACC GAG Ser Ala Glu Gln Met Thr Phe Thr Gln Thr Pro Gly Ala Glu Thr Glu 505 510 515	7244
GCA CCT GCC CAG ACC CCG AGC ACG ATA CCC GAG ATA TTT ACT CAG TCT Ala Pro Ala Gln Thr Pro Ser Thr Ile Pro Glu Ile Phe Thr Gln Ser 520 525 530	7292
CGT AGC ACG CCC CCC GAA ACC GCT CGC GCT CCG AGC GCG GCG CCG GAG Arg Ser Thr Pro Pro Glu Thr Ala Arg Ala Pro Ser Ala Ala Pro Glu 535 540 545	7340
GTT TTT ACA CAG AGT TCG AGT ACG GTA ACG GAG GTG TTT ACT CAG ACC Val Phe Thr Gln Ser Ser Ser Thr Val Thr Glu Val Phe Thr Gln Thr 550 555 560	7388
CCG AGC ACG GTA CCG AAA ACT ACT CTG AGT TCG AGT ACT GAA CCG GCG Pro Ser Thr Val Pro Lys Thr Thr Leu Ser Ser Thr Glu Pro Ala 565 570 575 580	7436
ATT TTT ACT CCG ACT CAG AGC GCG GGA ACT GAG GCC TTT ACT CAG ACT Ile Phe Thr Arg Thr Gln Ser Ala Gly Thr Glu Ala Phe Thr Gln Thr 585 590 595	7484
TCG AGT GCC GAG CCG GAC ACT ATG CGA ACT CAG AGT ACT GAA ACA CAC Ser Ser Ala Glu Pro Asp Thr Met Arg Thr Gln Ser Thr Glu Thr His 600 605 610	7532
TTT TTC ACT CAG GCC CCG AGT ACG GTA CCG AAA GCT ACT CAG ACT CCG Phe Phe Thr Gln Ala Pro Ser Thr Val Pro Lys Ala Thr Gln Thr Pro 615 620 625	7580
AGT ACA GAG CCG GAG GTG TTG ACT CAG AGT CCG AGT ACC GAA CCT GTG Ser Thr Glu Pro Glu Val Leu Thr Gln Ser Pro Ser Thr Glu Pro Val 630 635 640	7628
CCT TTC ACC CCG ACT CTG GGC GCA GAG CCG GAA ATT ACT CAG ACC CCG Pro Phe Thr Arg Thr Leu Gly Ala Glu Pro Glu Ile Thr Gln Thr Pro 645 650 655 660	7676
AGC GCG GCA CCG GAG GTT TAT ACT CCG AGT TCG AGT ACG ATG CCA GAA Ser Ala Ala Pro Glu Val Tyr Thr Arg Ser Ser Ser Thr Met Pro Glu 665 670 675	7724
ACT GCA CAG AGC ACA CCC CTG GCC TCG CAA AAC CCT ACC AGT TCG GGA Thr Ala Gln Ser Thr Pro Leu Ala Ser Gln Asn Pro Thr Ser Ser Gly 680 685 690	7772
ACC GGG ACG CAT AAT ACT GAA CCG AGG ACT TAT CCA GTG CAA ACG ACA Thr Gly Thr His Asn Thr Glu Pro Arg Thr Tyr Pro Val Gln Thr Thr 695 700 705	7820

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CCA CAT ACC CAG AAA CTC TAC ACA GAA AAT AAG ACT TTA TCG TTT CCT Pro His Thr Gln Lys Leu Tyr Thr Glu Asn Lys Thr Leu Ser Phe Pro 710 715 720	7868
ACT GTT GTT TCA GAA TTC CAT GAG ATG TCG ACG GCA GAG TCG CAG ACG Thr Val Val Ser Glu Phe His Glu Met Ser Thr Ala Glu Ser Gln Thr 725 730 735 740	7916
CCC CTA TTG GAC GTC AAA ATT GTA GAG GTG AAG TTT TCA AAC GAT GGC Pro Leu Leu Asp Val Lys Ile Val Glu Val Lys Phe Ser Asn Asp Gly 745 750 755	7964
GAA GTA ACG GCG ACT TGC GTT TCC ACC GTC AAA TCT CCC TAT AGG GTA Glu Val Thr Ala Thr Cys Val Ser Thr Val Lys Ser Pro Tyr Arg Val 760 765 770	8012
GAA ACT AAT TGG AAA GTA GAC CTC GTA GAT GTA ATG GAT GAA ATT TCT Glu Thr Asn Trp Lys Val Asp Leu Val Asp Val Met Asp Glu Ile Ser 775 780 785	8060
GGG AAC AGT CCC GCC GGG GTT TTT AAC AGT AAT GAG AAA TGG CAG AAA Gly Asn Ser Pro Ala Gly Val Phe Asn Ser Asn Glu Lys Trp Gln Lys 790 795 800	8108
CAG CTG TAC TAC AGA GTA ACC GAT GGA AGA ACA TCG GTC CAG CTA ATG Gln Leu Tyr Tyr Arg Val Thr Asp Gly Arg Thr Ser Val Gln Leu Met 805 810 815 820	8156
TGC CTG TCG TGC ACG AGC CAT TCT CCG GAA CCT TAC TGT CTT TTC GAC Cys Leu Ser Cys Thr Ser His Ser Pro Glu Pro Tyr Cys Leu Asp 825 830 835	8204
ACG TCT CTT ATA GCG AGG GAA AAA GAT ATC GCG CCA GAG TTA TAC TTT Thr Ser Leu Ile Ala Arg Glu Lys Asp Ile Ala Pro Glu Leu Tyr Phe 840 845 850	8252
ACC TCT GAT CCG CAA ACG GCA TAC TGC ACA ATA ACT CTG CCG TCC GGC Thr Ser Asp Pro Gln Thr Ala Tyr Cys Thr Ile Thr Leu Pro Ser Gly 855 860 865	8300
GTT GTT CCG AGA TTC GAA TGG AGC CTT AAT AAT GTT TCA CTG CCG GAA Val Val Pro Arg Phe Glu Trp Ser Leu Asn Asn Val Ser Leu Pro Glu 870 875 880	8348
TAT TTG ACG GCC ACG ACC GTT GTT TCG CAT ACC GCT GGC CAA AGT ACA Tyr Leu Thr Ala Thr Thr Val Val Ser His Thr Ala Gly Gln Ser Thr 885 890 895 900	8396
GTG TGG AAG AGC AGC GCG AGA GCA GGC GAG GCG TGG ATT TCT GGC CCG Val Trp Lys Ser Ser Ala Arg Ala Gly Glu Ala Trp Ile Ser Gly Arg 905 910 915	8444
GGA GGC AAT ATA TAC GAA TGC ACC GTC CTC ATC TCA GAC GGC ACT CGC Gly Gly Asn Ile Tyr Glu Cys Thr Val Leu Ile Ser Asp Gly Thr Arg 920 925 930	8492
GTT ACT ACG CGA AAG GAG AGG TGC TTA ACA AAC ACA TGG ATT GCG GTG Val Thr Thr Arg Lys Glu Arg Cys Leu Thr Asn Thr Trp Ile Ala Val 935 940 945	8540
GAA AAC GGT GCT GCT CAG GCG CAG CTG TAT TCA CTC TTT TCT GGA CTT Glu Asn Gly Ala Ala Gln Ala Gln Leu Tyr Ser Leu Phe Ser Gly Leu 950 955 960	8588
GTG TCA GGA TTA TGC GGG AGC ATA TCT GCT TTG TAC GCA ACG CTA TGG Val Ser Gly Leu Cys Gly Ser Ile Ser Ala Leu Tyr Ala Thr Leu Trp 965 970 975 980	8636

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ACC GCC ATT TAT TTT TGAGGAATGC TTTTGGACT ATCGTACTGC TTTCTTCCTT 8691
 Thr Ala Ile Tyr Phe
 985

CGCTAGCCAG AGCACCGCCG CCGTCACGTA CGACTACATT TTAGGCCGTC GCGCGCTCGA 8751

CGCGCTAACC ATACCGGGCG TTGGCCCGTA TAACAGATAC CTCACTAGGG TATCAAGAGG 8811

CTGCGACGTT GTGAGCTCA ACCCGATTTC TAACGTGGAC GACATGATAT CCGCGGCCAA 8871

AGAAAAAGAG AAGGGGGGCC CTTTCGAGSC CTCGTCGTC TGGTTCTACG TGATTAAGGG 8931

CGACGACGGC GAGGACAAGT ACTGTCCAAT CTATAGAAAA GAGTACAGGG AATGTGGCGA 8991

CGTACAACTG CTATCTGAAT GCGCCGTTC AATGTGCACAG ATGTGGGCGAG TGGACTATGT 9051

TCCTAGCACC CTTGTATGCG GAAATGGCGC GGGACTGACT ATATTCTCCC CCACGTCTGC 9111

GCTCTCTGGC CAATACTTGC TGACCCTGAA AATCGGAGA TTTGCGCAA CAGCTCTCGT 9171

AACCTAGAA GTTAACGATC GCTGTTTAAA GATCGGGTCG CAGCTTAACT TTTTACCSTC 9231

GAAATGCTGG ACAACAGAAC AGTATCAGAC TGGATTTCAA GCGGAACACC TTTATCCGAT 9291

CGCAGACACC AATACACGAC ACGCGGACGA CGTATATCGG GGATACGAAG ATATTCTGCA 9351

GCGCTGGAAT AATTTGCTGA GAAAAAGAA TCCTAGCGCG CCAGACCCCT GTCCAGATAG 9411

CGTCCCGCAA GAAATTCCTG CTGTAACCAA GAAACCGGAA GGGCGCACCC CGGACGCGA 9471

AAGCAGCGAA AAGAAGGCC CTCCAGAAGA CTCGAGGAGC GACATGCAGG CAGAGGCTTC 9531

TGGAGAAAAAT CCTGCCGCC TCCTCGAAGA CGACGAAGTC CCCGAGGACA CCGAGCACGA 9591

TGATCCAAC TCGGATCCTG ACTATTACAA TGACATGCCC GCGGTGATCC CGGTGGAGGA 9651

GACTACTAAA AGTTCTAATG CCGTCTCCAT GCCCATATTC GCGCGGTTTC TAGCCTGCGC 9711

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CCTAGAATAG GTGGTTTCTT CCTACATGCC ACGCCTCACG CTCATAATAT AAATCACATG 9831

GAATAGCATA CCAATGCCTA TTCATTGGGA CGTTCGAAAA GC 9873

ATG GCA TCG CTA CTT GGA ACT 9894
 Met Ala Ser Leu Leu Gly Thr
 1 5

CTG GCT CTC CTT GCC GCG ACG CTC GCA CCC TTC GGC GCG ATG GGA ATC 9942
 Leu Ala Leu Leu Ala Ala Thr Leu Ala Pro Phe Gly Ala Met Gly Ile
 10 15 20

GTG ATC ACT GGA AAT CAC GTC TCC GCC AGG ATT GAC GAC GAT CAC ATC 9990
 Val Ile Thr Gly Asn His Val Ser Ala Arg Ile Asp Asp Asp His Ile
 25 30 35

GTG ATC GTC GCG CTT CGC CCC GAA GCT ACA ATT CAA CTG CAG CTA TTT 10038
 Val Ile Val Ala Pro Arg Pro Glu Ala Thr Ile Gln Leu Gln Leu Phe
 40 45 50 55

TTC ATG CCT GGC CAG AGA CCC CAC AAA CCC TAC TCA GGA ACC GTC CGC 10086
 Phe Met Pro Gly Gln Arg Pro His Lys Pro Tyr Ser Gly Thr Val Arg
 60 65 70

GTC GCG TTT CGG TCT GAT ATA ACA AAC CAG TGC TAC CAG GAA CTT AGC 10134
 Val Ala Phe Arg Ser Asp Ile Thr Asn Gln Cys Tyr Gln Glu Leu Ser
 75 80 85

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GAG GAG CGC TTT GAA AAT TGC ACT CAT CGA TCG TCT TCT GTT TTT GTC Glu Glu Arg Phe Glu Asn Cys Thr His Arg Ser Ser Val Phe Val 90 95 100	10182
GGC TGT AAA GTG ACC GAG TAC ACG TTC TCC GCC TCG AAC AGA CTA ACC Gly Cys Lys Val Thr Glu Tyr Thr Phe Ser Ala Ser Asn Arg Leu Thr 105 110 115	10230
GGA CCT CCA CAC CCG TTT AAG CTC ACT ATA CGA AAT CCT CGT CCG AAC Gly Pro Pro His Pro Phe Lys Leu Thr Ile Arg Asn Pro Arg Pro Asn 120 125 130 135	10278
GAC AGC GGG ATG TTC TAC GTA ATT GTT CGG CTA GAC GAC ACC AAA GAA Asp Ser Gly Met Phe Tyr Val Ile Val Arg Leu Asp Asp Thr Lys Glu 140 145 150	10326
CCC ATT GAC GTC TTC GCG ATC CAA CTA TCG GTG TAT CAA TTC GCG AAC Pro Ile Asp Val Phe Ala Ile Gln Ser Val Tyr Gln Phe Ala Asn 155 160 165	10374
ACC GCC GCG ACT CGC GGA CTC TAT TCC AAG GCT TCG TGT CGC ACC TTC Thr Ala Ala Thr Arg Gly Leu Tyr Ser Lys Ala Ser Cys Arg Thr Phe 170 175 180	10422
GGA TTA CCT ACC GTC CAA CTT GAG GCC TAT CTC AGG ACC GAG GAA AGT Gly Leu Pro Thr Val Gln Leu Glu Ala Tyr Leu Arg Thr Glu Glu Ser 185 190 195	10470
TGG CGC AAC TGG CAA GCG TAC GTT GCC ACG GAG GCC ACG ACG ACC AGC Trp Arg Asn Trp Gln Ala Tyr Val Ala Thr Glu Thr Thr Thr Ser 200 205 210 215	10518
GCC GAG GCG ACA ACC CCG ACG CCC GTC ACT GCA ACC AGC GCC TCC GAA Ala Glu Ala Thr Thr Pro Thr Pro Val Thr Ala Thr Ser Ala Ser Glu 220 225 230	10566
CTT GAA GCG GAA CAC TTT ACC TTT CCC TGG CTA GAA AAT GGC GTG GAT Leu Glu Ala Glu His Phe Thr Phe Pro Trp Leu Glu Asn Gly Val Asp 235 240 245	10614
CAT TAC GAA CCG ACA CCC GCA AAC GAA AAT TCA AAC GTT ACT GTC CGT His Tyr Glu Pro Thr Pro Ala Asn Glu Asn Ser Asn Val Thr Val Arg 250 255 260	10662
CTC GGG ACA ATG AGC CCT ACG CTA ATT GGG GTA ACC GTG GCT GCC GTC Leu Gly Thr Met Ser Pro Thr Leu Ile Gly Val Thr Val Ala Ala Val 265 270 275	10710
GTG AGC GCA ACG ATC GGC CTC GTC ATT GTA ATT TCC ATC GTC ACC AGA Val Ser Ala Thr Ile Gly Leu Val Ile Val Ile Ser Ile Val Thr Arg 280 285 290 295	10758
AAC ATG TGC ACC CCG CAC CGA AAA TTA GAC ACG GTC TCG CAA GAC GAC Asn Met Cys Thr Pro His Arg Lys Leu Asp Thr Val Ser Gln Asp Asp 300 305 310	10806
GAA GAA CGT TCC CAA ACT AGA AGG GAA TCG CGA AAA TTT GGA CCC ATG Glu Glu Arg Ser Gln Thr Arg Arg Glu Ser Arg Lys Phe Gly Pro Met 315 320 325	10854
GTT GCG TGC GAA ATA AAC AAG GGC GCT GAC CAG GAT AGT GAA CTT GTG Val Ala Cys Glu Ile Asn Lys Gly Ala Asp Gln Asp Ser Glu Leu Val 330 335 340	10902
GAA CTG GTT GCG ATT GTT AAC CCG TCT GCG CTA AGC TCG CCC GAC TCA Glu Leu Val Ala Ile Val Asn Pro Ser Ala Leu Ser Ser Pro Asp Ser 345 350 355	10950

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ATA AAA ATG TGATTAAGTC TGAATGTGGC TCTCCAATCA TTTCGATTCT Ile Lys Met 360	10999
CTAATCTCCC AATCCTCTCA AAGAGGGGACG TATCGGACAC GGACTGGGAG GGGCGTACTA	11059
CACGATAGTT ATATGGTACA GCAGAGGCCCT CTGAACACTT AGGAGGAGAA TTCAGCCGGG	11119
GAGAGCCCCT GTTGAGTAGG CTGGGAGCA TATTGCAGG ATG AAC ATG TTA GTG Met Asn Met Leu Val 1 5	11173
ATA GTT CTC GCC TCT TGT CTT GCG CGC CTA ACT TTT GCG ACG CGA CAC Ile Val Leu Ala Ser Cys Leu Ala Arg Leu Thr Phe Ala Thr Arg His 10 15 20	11221
GTC CTC TTT TTG GAA GGC ACT CAG GCT GTC CTC GGG GAA GAT GAT CCC Val Leu Phe Leu Glu Gly Thr Gln Ala Val Leu Gly Glu Asp Asp Pro 25 30 35	11269
AGA AAC GTT CCG GAA GGG ACT GTA ATC AAA TGG ACA AAA GTC CTG CGG Arg Asn Val Pro Glu Gly Thr Val Ile Lys Trp Thr Lys Val Leu Arg 40 45 50	11317
AAC GCG TGC AAG ATG AAG GCG GCC GAT GTC TGC TCT TCG CCT AAC TAT Asn Ala Cys Lys Met Lys Ala Ala Asp Val Cys Ser Ser Pro Asn Tyr 55 60 65	11365
TGC TTT CAT GAT TTA ATT TAC GAC GGA GGA AAG AAA GAC TGC CCG CCC Cys Phe His Asp Leu Ile Tyr Asp Gly Gly Lys Lys Asp Cys Pro Pro 70 75 80 85	11413
GCG GGA CCC CTG TCT GCA AAC CTG GTA ATT TTA CTA AAG GCG GAA Ala Gly Pro Leu Ser Ala Asn Leu Val Ile Leu Leu Lys Arg Gly Glu 90 95 100	11461
AGC TTC GTC GTG CTG GGT TCT GGG CTA CAC AAC AGC AAT ATA ACT AAT Ser Phe Val Val Leu Gly Ser Gly Leu His Asn Ser Asn Ile Thr Asn 105 110 115	11509
ATC ATG TGG ACA GAG TAC GGA GGC CTG CTC TTT GAT CCT GTA ACT CGT Ile Met Trp Thr Glu Tyr Gly Gly Leu Leu Phe Asp Pro Val Thr Arg 120 125 130	11557
TCG GAC GAG GGA ATC TAT TTT CGA CGG ATC TCT CAG CCA GAT CTG GCC Ser Asp Glu Gly Ile Tyr Phe Arg Arg Ile Ser Gln Pro Asp Leu Ala 135 140 145	11605
ATG GAA ACT ACA TCG TAC AAC GTC AGC GTT CTT TCG CAC GTA GAC GAG Met Glu Thr Thr Ser Tyr Asn Val Ser Val Leu Ser His Val Asp Glu 150 155 160 165	11653
AAG GCT CCA GCA CCG CAC GAG GTG GAG ATA GAC ACC ATC AAG CCG TCA Lys Ala Pro Ala Pro His Glu Val Glu Ile Asp Thr Ile Lys Pro Ser 170 175 180	11701
GAG GCC CAC GCG CAC GTG GAA TTA CAA ATG CTG CCG TTT CAT GAA CTC Glu Ala His Ala His Val Glu Leu Gln Met Leu Pro Phe His Glu Leu 185 190 195	11749
AAC GAC AAC AGC CCC ACC TAT GTG ACC CCT GTT CTT AGA GTC TTC CCA Asn Asp Asn Ser Pro Thr Tyr Val Thr Pro Val Leu Arg Val Phe Pro 200 205 210	11797
CCG ACC GAG CAC GTA AAA TTT AAC GTT ACG TAT TCG TGS TAT GGG TTT Pro Thr Glu His Val Lys Phe Asn Val Thr Tyr Ser Trp Tyr Gly Phe 215 220 225	11845

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GAT Asp 230	GTC Val Lys	AAA Glu Glu	GAG Glu Glu	GAG Cys 235	TGC Glu Glu	GAA Glu Glu	GAA Glu Glu	GTG Val Lys	CTG Leu Phe	TTC Glu Pro	GAG Glu Cys	CCG Pro Val	TGC Cys Val	GTA Val 245	11893
TAC Tyr 230	CAT His Pro	CCT Pro Thr	ACA Thr 250	GAC Gly 250	GGC Lys Cys	AAA Lys Cys	TGT Gln 255	CAG Gln 255	TTT Pro Ala	GCA Ala Thr	ACC Asn Gln	AAC Gln 260	CAG Gln Arg	AGA Arg 260	11941
TGC Cys 265	CTC Leu Ile	ATA Gly 265	GGA Ser Val	TCT Val 265	GTC Leu Met	TTG Leu Met	ATG Ala Glu	GCG Ala Glu	GAA Phe 270	TTC Phe 270	TTG Leu Gly	GGC Ala 275	GCC Ala Ser	TCT Ser 275	11989
TTG Leu 280	CTG Leu 280	GAT Cys Ser	TGT Ser Arg	TCC Arg 285	CGC Asp Thr	GAT Asp 285	ACT Thr 285	CTA Leu Glu	GAA Glu 290	GAC Asp Cys	TGC Cys His	CAC Glu 290	GAA Asn Arg	AAT Arg 290	12037
GTG Val 295	CCG Pro Asn	AAC Leu Arg	CTA Arg Phe	CGG Phe 300	TTC Asp Ser	GAT Ser Arg	TCG Arg Leu	CGA Ser Leu	CTC Ser 305	TCC Ser 305	GAG Ser Arg	TCA Ser Ala	CGC Ala Gly	GGC Gly 305	12085
CTG Leu 310	GTG Val Ile	ATC Ile Ser	AGT Ser Pro	CCT Pro 315	CTT Leu Ile	ATA Ile Ala	GCC Ile Ala	ATC Ile Pro	CCC Val 320	AAA Val Leu	GTT Ile Ile	TTG Ile Ile	ATA Ile Val	GTC Val 325	12133
GTT Val 330	TCC Ser Asp	GAC Gly 330	GGA Ile 330	GAC Ile 330	ATT Ile 330	TTG Leu Gly	GGA Trp 335	TGG Trp 335	AGC Ser Tyr	TAC Thr Val	ACG Thr Val	GTG Val Leu	CTC Gly Lys	AAA Lys 340	12181
CGT Arg 345	AAC Asn Ser	AGT Ser 345	CCG Val 345	CGC Val 345	GTA Val 345	GTA Val 345	GTC Val 345	GAA Val 345	ACG Thr His	CAC Met Pro	ATG Met Pro	CCC Ser Lys	TCG Lys Val	AAG Val 355	12229
CCG Pro 360	ATG Met 360	AAC Asn Lys	AAA Val 360	GTA Val 360	GTA Val 360	ATT Ile 365	GGC Gly 365	AGT Ser 365	CCC Pro 370	GGA Pro 370	CCA Pro 370	ATG Met Asp	GAC Glu Thr	ACG Thr 370	12277
GGT Gly 375	AAC Asn Tyr	TAT Tyr Lys	AAA Lys 375	ATG Lys 375	TAC Met 375	TTC Phe 380	GTC Val 380	GTC Val 380	GCG Val 385	GGG Val 385	GTG Val 385	GCC Val 385	GCG Ala Thr	ACG Cys 385	12325
GTA Val 390	ATT Ile Leu	CTT Leu Thr	ACA Thr Cys	TGC Ala 395	GCT Ala 395	CTG Leu	CTT Leu	GTG Val	GGG Val	AAA Gly	AAG Lys	AAG Lys	TGC Lys	CCC Pro	12373
CAC His 410	CAA Gln Met	ATG Met Gly	GGT Thr Phe	ACT Thr 410	TTT Thr Phe	TCC Ser	AAG Lys	ACC Thr	GAA Glu	CCA Pro	TTG Leu	TAC Tyr	GCG Ala	CCG Pro	12421
CCC Pro 425	AAA Lys Asn	AAC Glu Phe	GAG Glu 425	TTT Glu 425	GAG Ala Gly	GCC Ala Gly	GGC Glu 430	GGG Glu 430	CTT Leu Thr	ACG Thr Asp	GAC Asp 435	GAT Glu 435	GAG Glu Val	GTG Val 435	12469
ATT Ile 440	TAT Tyr Asp	GAC Glu Val	GAA Val Tyr	GTA Tyr 440	TAC Glu 445	GAA Glu 445	CCC Pro 445	CTA Leu Phe	TTT Phe Arg	CGC Gly Tyr	GGC Gly Cys	TAC Tyr Lys	TGT Lys Gln	AAG Gln 450	12517
GAA Glu 455	TTC Phe Arg	CGC Glu Asp	GAA Val 455	GAT Val 460	GTG Thr 460	AAT Thr 460	ACC Phe 460	TTT Phe 465	TTC Phe Gly	GGT Ala Val	GCG Val 465	GTC Val 465	GTG Glu Gly	GGA Gly 465	12565
GAA Glu 470	AGG Arg Ala	GCC Ala Leu	TTA Asn Phe	AAC Phe 475	TTT Lys 475	AAA Ser 475	TCC Ala 480	GCC Ile 480	ATC Ala Ser	GCA Met Ala	TCA Met Ala	ATG Asp Arg	GCA Asp Arg	CGC Arg 485	12613
ATC Ile 490	CTG Leu Ala	GCA Ala Asn	AAT Lys Ser	AAA Lys 490	AGC Ser 490	GGC Ser 490	AGA Arg 495	AGG Met 495	AAT Met 495	ATG Met 495	GAT Met 495	AGC Ser 500	TAT Ser 500	TAGTTGGTC Tyr 500	12664

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ATG CCT TTT AAG ACC AGA GGG GCC GAA GAC	12694
Met Pro Phe Lys Thr Arg Gly Ala Glu Asp	
1 5 10	
GCG GCC GCG GGC AAG AAC AGG TTT AAG AAA TCG AGA AAT CGG GAA ATC	12742
Ala Ala Ala Gly Lys Asn Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile	
15 20 25	
TTA CCG ACC AGA CTG CGT GGC ACC GGT AAG AAA ACT GCC GGA TTG TCC	12790
Leu Pro Thr Arg Leu Arg Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser	
30 35 40	
AAT TAT ACC CAG CCT ATT CCC TGG AAC CCT AAA TTC TGC AGC GCG CGC	12838
Asn Tyr Thr Gln Pro Ile Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg	
45 50 55	
GGG GAA TCT GAC AAC CAC GCG TGT AAA GAC ACT TTT TAT CGC AGG ACG	12886
Gly Glu Ser Asp Asn His Ala Cys Lys Asp Thr Phe Tyr Arg Arg Thr	
60 65 70	
TGC TGC GCA TCG CGC TCT ACC GTT TCC AGT CAA CCC GAT TCC CCC CAC	12934
Cys Cys Ala Ser Arg Ser Thr Val Ser Ser Gln Pro Asp Ser Pro His	
75 80 85 90	
ACA CCC ATG CCT ACT GAG TAT GGG CGC GTG CCC TCC GCA AAG CGC AAA	12982
Thr Pro Met Pro Thr Glu Tyr Gly Arg Val Pro Ser Ala Lys Arg Lys	
95 100 105	
AAA CTA TCA TCT TCA GAC TSS GAG GGC GCG CAC CAA CCC CTA GTA TCC	13030
Lys Leu Ser Ser Ser Asp Xaa Glu Gly Ala His Gln Pro Leu Val Ser	
110 115 120	
TGT AAA CTT CCG GAT TCT CAA GCA GCA CCG GCG CGA ACC TAT AGT TCT	13078
Cys Lys Leu Pro Asp Ser Gln Ala Ala Pro Ala Arg Thr Tyr Ser Ser	
125 130 135	
GCG CAA AGA TAT ACT GTT GAC GAG GTT TCG TCG CCA ACT CCG CCA GGC	13126
Ala Gln Arg Tyr Thr Val Asp Glu Val Ser Ser Pro Thr Pro Pro Gly	
140 145 150	
GTC GAC GCT GTT GCG GAC TTA GAA ACG GCG GCG GAA CTT CCT GGC GCT	13174
Val Asp Ala Val Ala Asp Leu Glu Thr Arg Ala Glu Leu Pro Gly Ala	
155 160 165 170	
ACG ACG GAA CAA ACG GAA AGT AAA AAT AAG CTC CCC AAC CAA CAA TCG	13222
Thr Thr Glu Gln Thr Glu Ser Lys Asn Lys Leu Pro Asn Gln Gln Ser	
175 180 185	
CGC CTG AAG CCG AAA CCC ACA AAC GAG CAC GTC GGA GGG GAG CGG TGC	13270
Arg Leu Lys Pro Lys Pro Thr Asn Glu His Val Gly Gly Glu Arg Cys	
190 195 200	
CCC TCC GAA GGC ACG GTC GAG GCG CCA TCG CTC GGC ATC CTC TCG CGC	13318
Pro Ser Glu Gly Thr Val Glu Ala Pro Ser Leu Gly Ile Leu Ser Arg	
205 210 215	
GTC GGG GCA GCG ATA GCA AAC GAG CTG GCT CGT ATG CGG AGG GCG TGT	13366
Val Gly Ala Ala Ile Ala Asn Glu Leu Ala Arg Met Arg Arg Ala Cys	
220 225 230	
CTT CCG CTC GCC GCG TCG GCG GCC GCT GCC GGA ATA GTG GCC TGG GCC	13414
Leu Pro Leu Ala Ala Ser Ala Ala Ala Gly Ile Val Ala Trp Ala	
235 240 245 250	
GCG GCG AGG GCC TTG CAG AAA CAA GGG CGG TAG CAGTAATAATA ACCACACAA	13467
Ala Ala Arg Ala Leu Gln Lys Gln Gly Arg *	
255 260	

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Met	Arg	Phe	Arg	Arg	5	Ile	Cys	Ser	Arg	Ser	Arg	Ala	Glu	Lys	Arg	Arg
Arg	Thr	Thr	Glu	Asn	Pro	Leu	Thr	Ser	Lys	Arg	Val	Cys	Val	Leu	Asp	
Ser	Phe	Ser	Arg	Thr	Met	Ser	Leu	Arg	Pro	Tyr	Ala	Glu	Ile	Leu	Pro	
Thr	Ala	Glu	Gly	Val	Glu	Arg	Leu	Ala	Glu	Leu	Val	Ser	Val	Thr	Met	
Thr	Thr	Arg	Ala	Glu	Pro	Val	Thr	Glu	Asn	Thr	Ala	Val	Asn	Ser	Ile	
Pro	Pro	Ala	Asn	Glu	Asn	Gly	Gln	Asn	Phe	Ala	Tyr	Ala	Gly	Asp	Gly	
Pro	Ser	Thr	Thr	Glu	Lys	Val	Asp	Gly	Ser	His	Thr	Asp	Phe	Asp	Glu	
Ala	Ser	Ser	Asp	Tyr	Ala	Gly	Pro	Val	Pro	Leu	Ala	Gln	Thr	Arg	Leu	
Lys	His	Ser	Ser	Glu	Phe	Leu	Gln	His	Phe	Arg	Val	Leu	Asp	Asp	Leu	
Val	Glu	Gly	Ala	Tyr	Gly	Phe	Ile	Cys	Gly	Val	Arg	Arg	Tyr	Thr	Glu	
Glu	Glu	Gln	Arg	Arg	Arg	Gly	Val	Asn	Ser	Thr	Asn	Gln	Gly	Lys	Ser	
Lys	Cys	Lys	Arg	Leu	Ile	Ala	Lys	Tyr	Val	Lys	Asn	Gly	Thr	Arg	Ala	
Ala	Ser	Gln	Leu	Glu	Asn	Glu	Ile	Leu	Val	Leu	Gly	Arg	Leu	Asn	His	
Glu	Asn	Val	Leu	Lys	Ile	Gln	Glu	Ile	Leu	Arg	Tyr	Pro	Asp	Asn	Thr	
Tyr	Met	Leu	Thr	Gln	Arg	Tyr	Gln	Phe	Asp	Leu	Tyr	Ser	Tyr	Met	Tyr	
Asp	Glu	Ala	Phe	Asp	Trp	Lys	Asp	Ser	Pro	Met	Leu	Lys	Gln	Thr	Arg	
Arg	Ile	Met	Lys	Gln	Leu	Met	Ser	Ala	Val	Ser	Tyr	Ile	His	Ser	Lys	

Lys Leu Ile His Arg Asp Ile Lys Leu Glu Asn Ile Phe Leu Asn Cys
 275 280 285
 Asp Gly Lys Thr Val Leu Gly Asp Phe Gly Thr Val Thr Pro Phe Glu
 290 295 300
 Asn Glu Arg Glu Pro Phe Glu Tyr Gly Trp Val Gly Thr Val Ala Thr
 305 310 315 320
 Asn Ser Pro Glu Ile Leu Ala Arg Asp Ser Tyr Cys Glu Ile Thr Asp
 325 330 335
 Ile Trp Ser Cys Gly Val Val Leu Leu Glu Met Val Ser His Glu Phe
 340 345 350
 Cys Pro Ile Gly Asp Gly Gly Asp Asn Pro His Gln Gln Leu Leu Lys
 355 360 365
 Val Ile Asp Ser Leu Ser Val Cys Asp Glu Glu Phe Pro Asp Pro Pro
 370 375 380
 Cys Asn Leu Tyr Asn Tyr Leu His Tyr Ala Ser Ile Asp Arg Ala Gly
 385 390 395 400
 His Thr Val Pro Ser Leu Ile Arg Asn Leu His Leu Pro Ala Asp Val
 405 410 415
 Glu Tyr Pro Leu Val Lys Met Leu Thr Phe Asp Trp Arg Leu Arg Pro
 420 425 430
 Ser Ala Ala Glu Val Leu Ala Met Pro Leu Phe Ser Ala Glu Glu Glu
 435 440 445
 Arg Thr Ile Thr Ile Ile His Gly Lys His Lys Pro Ile Arg Pro Glu
 450 455 460
 Ile Arg Ala Arg Val Pro Arg Ser Met Ser Glu Gly
 465 470 475

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Leu Pro His Arg Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe
 1 5 10 15
 Cys Ser Val Phe Val Ile His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr
 20 25 30
 Asn Lys Thr Met Leu Leu Tyr Arg Pro Asp Ser Thr Met Arg His Ser
 35 40 45
 Gly Gly Asp Ala Asn His Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile
 50 55 60
 Gly Ala Phe Ser Ala Arg Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr
 65 70 75 80

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Glu Ser Ser Ser Ser Ser Asp Met Leu Asp Pro Phe Ser Thr Asp Lys
85 90 95

Glu Phe Gly Gly Lys Trp Thr Val Asp Gly Pro Ala Asp Ile Thr Ala
100 105 110

Glu Val Leu Ser Gln Ala Trp Asp Val Leu Gln Leu Val Lys His Glu
115 120 125

Asp Ala Glu Glu Glu Arg Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile
130 135 140

Gln Pro Phe Asn Ala Trp Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp
145 150 155 160

Phe Thr Arg Ala Pro Ile Val Tyr Pro Ser Ala Glu Val Leu Asp Ala
165 170 175

Glu Ala Leu Lys Val Gly Ala Phe Val Ser Arg Val Leu Gln Cys Val
180 185 190

Pro Phe Thr Arg Ser Lys Lys Ser Val Thr Val Arg Asp Ala Gln Ser
195 200 205

Phe Leu Gly Asp Ser Phe Trp Arg Ile Met Gln Asn Val Tyr Thr Val
210 215 220

Cys Leu Arg Gln His Ile Thr Arg Leu Arg His Pro Ser Ser Lys Ser
225 230 235 240

Ile Val Asn Cys Asn Asp Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe
245 250 255

His Trp Arg Gly Met Arg Val Pro Ser Leu Lys Leu Ala Ser Pro Pro
260 265 270

Glu Glu Asn Ile Gln His Gly Pro Met Ala Ala Val Phe Arg Asn Ala
275 280 285

Gly Ala Gly Leu Phe Leu Trp Pro Ala Met Arg Ala Ala Phe Glu Glu
290 295 300

Arg Asp Lys Arg Leu Leu Arg Ala Cys Leu Ser Ser Leu Asp Ile Met
305 310 315 320

Asp Ala Ala Val Leu Ala Ser Phe Pro Phe Tyr Trp Arg Gly Val Gln
325 330 335

Asp Thr Ser Arg Phe Glu Pro Ala Leu Gly Cys Leu Ser Glu Tyr Phe
340 345 350

Ala Leu Val Val Leu Leu Ala Glu Thr Val Leu Ala Thr Met Phe Asp
355 360 365

His Ala Leu Val Phe Met Arg Ala Leu Ala Asp Gly Asn Phe Asp Asp
370 375 380

Tyr Asp Glu Thr Arg Tyr Ile Asp Pro Val Lys Asn Glu Tyr Leu Asn
385 390 395 400

Gly Ala Glu Gly Thr Leu Leu Arg Gly Ile Val Ala Ser Asn Thr Ala
405 410 415

Leu Ala Val Val Cys Ala Asn Thr Tyr Ser Thr Ile Arg Lys Leu Pro
420 425 430

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Ser Val Ala Thr Ser Ala Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu
435 440 445
Lys Ala Arg Arg Pro Gly Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys
450 455 460
Glu Phe Phe Phe Tyr Ile Ala Trp Leu Gln Arg Val Ala Thr His Ala
465 470 475 480
Asn Phe Cys Leu Asn Ile Leu Lys Arg Ser Val Asp Thr Gly Pro Arg
485 490 495
His Phe Cys Ser Gly Pro Ala Arg Arg Ser Gly Cys Ser Ser
500 505 510

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Cys Pro Leu Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser Lys
1 5 10 15
Ala Met Gly Ser Glu Leu Lys Arg Glu Lys Leu Glu Thr Phe Val Lys
20 25 30
Ala Ile Ser Ser Asp Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu Ile
35 40 45
Ser Asp His Ala Arg Glu Ile Ile Ala Asp Gly Val Arg Phe Lys Pro
50 55 60
Val Ile Asp Glu Pro Val Arg Ala Ser Val Ala Leu Ser Thr Ala Ala
65 70 75 80
Ala Gly Lys Val Lys Ala Arg Arg Leu Thr Ser Val Arg Ala Pro Val
85 90 95
Pro Pro Ala Gly Ala Val Ser Ala Arg Arg Lys Ser Glu Ile
100 105 110

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Gly Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val
1 5 10 15
Cys Ser Leu Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly
20 25 30

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Leu Glu Ser Ser Pro Phe Pro Phe Gly Gly Lys Ile Ile Ala Gln Ala
35 40 45
Cys Asn Arg Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser
50 55 60
Gly Arg Thr Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn
65 70 75 80
Ser Asn Pro Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser
85 90 95
Gly His Glu Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn
100 105 110
Ala Ser Val Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys
115 120 125
Gln Cys Glu Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly
130 135 140
Ser Tyr Val Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr
145 150 155 160
Asp Ala Gly Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr
165 170 175
Thr Gly Ser Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp
180 185 190
Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu
195 200 205
Ser Ser Tyr Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu
210 215 220
Asp Tyr Ser Asn Cys Leu Asp Met Pro Pro Leu Arg Pro Trp Thr Thr
225 230 235 240
Val Cys Ser His Asp Val Glu Glu Gln Glu Asn Ala Thr Asp Glu Leu
245 250 255
Tyr Leu Trp Asp Glu Glu Cys Ala Gly Pro Leu Asp Glu Tyr Val Asp
260 265 270
Glu Arg Ser Glu Thr Met Pro Arg Met Val Val Phe Ser Pro Pro Ser
275 280 285
Thr Leu Gln Gln
290

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Thr Met Leu Val Leu Arg Leu Phe Leu Leu Ala Val Ala Asp
1 5 10 15

Ala Ala Leu Pro Thr Gly Arg Phe Cys Arg Val Trp Lys Val Pro Pro
20 25 30

Gly Gly Thr Ile Gln Glu Asn Leu Ala Val Leu Ala Glu Ser Pro Val
35 40 45

Thr Gly His Ala Thr Tyr Pro Pro Pro Glu Gly Ala Val Ser Phe Gln
50 55 60

Ile Phe Ala Asp Thr Pro Thr Leu Arg Ile Arg Tyr Gly Pro Thr Glu
65 70 75 80

Asp Glu Leu Ala Leu Glu Arg Gly Thr Ser Ala Ser Asp Ala Asp Asn
85 90 95

Val Thr Phe Ser Leu Ser Tyr Arg Pro Arg Pro Glu Ile His Gly Ala
100 105 110

Tyr Phe Thr Ile Gly Val Phe Ala Thr Gly Gln Ser Thr Glu Ser Ser
115 120 125

Tyr Ser Val Ile Ser Arg Val Leu Val Asn Ala Ser Leu Glu Arg Ser
130 135 140

Val Arg Leu Glu Thr Pro Cys Asp Glu Asn Phe Leu Gln Asn Glu Pro
145 150 155 160

Thr Trp Gly Ser Lys Arg Trp Leu Gly Pro Pro Ser Pro Tyr Val Arg
165 170 175

Asp Asn Asp Val Ala Val Leu Thr Lys Ala Gln Tyr Ile Gly Glu Cys
180 185 190

Tyr Ser Asn Ser Ala Ala Gln Thr Gly Leu Thr Ser Leu Asn Met Thr
195 200 205

Phe Phe Tyr Ser Pro Lys Arg Ile Val Asn Val Thr Trp Thr Thr Gly
210 215 220

Gly Pro Ser Pro Ser Arg Ile Thr Val Tyr Ser Ser Arg Glu Asn Gly
225 230 235 240

Gln Pro Val Leu Arg Asn Val Ser Asp Gly Phe Leu Val Lys Tyr Thr
245 250 255

Pro Asp Ile Asp Gly Arg Ala Met Ile Asn Val Ile Ala Asn Tyr Ser
260 265 270

Pro Ala Asp Ser Gly Ser Val Leu Ala Phe Thr Ala Phe Arg Glu Gly
275 280 285

Lys Leu Pro Ser Ala Ile Gln Leu His Arg Ile Asp Met Ser Gly Thr
290 295 300

Glu Pro Pro Gly Thr Glu Thr Thr Phe Asp Cys Gln Lys Met Ile Glu
305 310 315 320

Thr Pro Tyr Arg Ala Leu Gly Ser Asn Val Pro Arg Asp Asp Ser Ile
325 330 335

Arg Pro Gly Ala Thr Leu Pro Pro Phe Asp Thr Ala Ala Pro Asp Phe
340 345 350

Asp Thr Gly Thr Ser Pro Thr Pro Thr Thr Val Pro Glu Pro Ala Ile
355 360 365

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Thr Thr Leu Ile Pro Arg Ser Thr Thr Ser Asp Met Gly Phe Phe Ser Thr
370 375 380

Ala Arg Ala Thr Gly Ser Glu Thr Leu Ser Val Pro Val Gln Glu Thr
385 390 395 400

Asp Arg Thr Leu Ser Thr Thr Pro Leu Thr Leu Pro Leu Thr Pro Gly
405 410 415

Glu Ser Glu Asn Thr Leu Phe Pro Thr Thr Ala Pro Gly Ile Ser Thr
420 425 430

Glu Thr Pro Ser Ala Ala His Glu Thr Thr Gln Thr Gln Ser Ala Glu
435 440 445

Thr Val Val Phe Thr Gln Ser Pro Ser Thr Glu Ser Glu Thr Ala Arg
450 455 460

Ser Gln Ser Gln Glu Pro Trp Tyr Phe Thr Gln Thr Pro Ser Thr Glu
465 470 475 480

Gln Ala Ala Leu Thr Gln Thr Gln Ile Ala Glu Thr Glu Ala Leu Phe
485 490 495

Thr Gln Thr Pro Ser Ala Glu Gln Met Thr Phe Thr Gln Thr Pro Gly
500 505 510

Ala Glu Thr Glu Ala Pro Ala Gln Thr Pro Ser Thr Ile Pro Glu Ile
515 520 525

Phe Thr Gln Ser Arg Ser Thr Pro Pro Glu Thr Ala Arg Ala Pro Ser
530 535 540

Ala Ala Pro Glu Val Phe Thr Gln Ser Ser Ser Thr Val Thr Glu Val
545 550 555 560

Phe Thr Gln Thr Pro Ser Thr Val Pro Lys Thr Thr Leu Ser Ser Ser
565 570 575

Thr Glu Pro Ala Ile Phe Thr Arg Thr Gln Ser Ala Gly Thr Glu Ala
580 585 590

Phe Thr Gln Thr Ser Ser Ala Glu Pro Asp Thr Met Arg Thr Gln Ser
595 600 605

Thr Glu Thr His Phe Phe Thr Gln Ala Pro Ser Thr Val Pro Lys Ala
610 615 620

Thr Gln Thr Pro Ser Thr Glu Pro Glu Val Leu Thr Gln Ser Pro Ser
625 630 635 640

Thr Glu Pro Val Pro Phe Thr Arg Thr Leu Gly Ala Glu Pro Glu Ile
645 650 655

Thr Gln Thr Pro Ser Ala Ala Pro Glu Val Tyr Thr Arg Ser Ser Ser
660 665 670

Thr Met Pro Glu Thr Ala Gln Ser Thr Pro Leu Ala Ser Gln Asn Pro
675 680 685

Thr Ser Ser Gly Thr Gly Thr His Asn Thr Glu Pro Arg Thr Tyr Pro
690 695 700

Val Gln Thr Thr Pro His Thr Gln Lys Leu Tyr Thr Glu Asn Lys Thr
705 710 715 720

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Leu Ser Phe Pro Thr Val Val Ser Glu Phe His Glu Met Ser Thr Ala
 725 730 735
 Glu Ser Gln Thr Pro Leu Leu Asp Val Lys Ile Val Glu Val Lys Phe
 740 745 750
 Ser Asn Asp Gly Glu Val Thr Ala Thr Cys Val Ser Thr Val Lys Ser
 755 760 765
 Pro Tyr Arg Val Glu Thr Asn Trp Lys Val Asp Leu Val Asp Val Met
 770 775 780
 Asp Glu Ile Ser Gly Asn Ser Pro Ala Gly Val Phe Asn Ser Asn Glu
 785 790 795 800
 Lys Trp Gln Lys Gln Leu Tyr Tyr Arg Val Thr Asp Gly Arg Thr Ser
 805 810 815
 Val Gln Leu Met Cys Leu Ser Cys Thr Ser His Ser Pro Glu Pro Tyr
 820 825 830
 Cys Leu Phe Asp Thr Ser Leu Ile Ala Arg Glu Lys Asp Ile Ala Pro
 835 840 845
 Glu Leu Tyr Phe Thr Ser Asp Pro Gln Thr Ala Tyr Cys Thr Ile Thr
 850 855 860
 Leu Pro Ser Gly Val Val Pro Arg Phe Glu Trp Ser Leu Asn Asn Val
 865 870 875 880
 Ser Leu Pro Glu Tyr Leu Thr Ala Thr Thr Val Val Ser His Thr Ala
 885 890 895
 Gly Gln Ser Thr Val Trp Lys Ser Ser Ala Arg Ala Gly Glu Ala Trp
 900 905 910
 Ile Ser Gly Arg Gly Gly Asn Ile Tyr Glu Cys Thr Val Leu Ile Ser
 915 920 925
 Asp Gly Thr Arg Val Thr Thr Arg Lys Glu Arg Cys Leu Thr Asn Thr
 930 935 940
 Trp Ile Ala Val Glu Asn Gly Ala Ala Gln Ala Gln Leu Tyr Ser Leu
 945 950 955 960
 Phe Ser Gly Leu Val Ser Gly Leu Cys Gly Ser Ile Ser Ala Leu Tyr
 965 970 975
 Ala Thr Leu Trp Thr Ala Ile Tyr Phe
 980 985

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ser Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr Leu Ala
 1 5 10 15

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Pro Phe Gly Ala Met Gly Ile Val Ile Thr Gly Asn His Val Ser Ala
20 30

Arg Ile Asp Asp Asp His Ile Val Ile Val Ala Pro Arg Pro Glu Ala
35 45

Thr Ile Gln Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro His Lys
50 55 60

Pro Tyr Ser Gly Thr Val Arg Val Ala Phe Arg Ser Asp Ile Thr Asn
65 70 75 80

Gln Cys Tyr Gln Glu Leu Ser Glu Glu Arg Phe Glu Asn Cys Thr His
85 90 95

Arg Ser Ser Ser Val Phe Val Gly Cys Lys Val Thr Glu Tyr Thr Phe
100 105 110

Ser Ala Ser Asn Arg Leu Thr Gly Pro Pro His Pro Phe Lys Leu Thr
115 120 125

Ile Arg Asn Pro Arg Pro Asn Asp Ser Gly Met Phe Tyr Val Ile Val
130 135 140

Arg Leu Asp Asp Thr Lys Glu Pro Ile Asp Val Phe Ala Ile Gln Leu
145 150 155

Ser Val Tyr Gln Phe Ala Asn Thr Ala Ala Thr Arg Gly Leu Tyr Ser
165 170 175

Lys Ala Ser Cys Arg Thr Phe Gly Leu Pro Thr Val Gln Leu Glu Ala
180 185 190

Tyr Leu Arg Thr Glu Glu Ser Trp Arg Asn Trp Gln Ala Tyr Val Ala
195 200 205

Thr Glu Ala Thr Thr Thr Ser Ala Glu Ala Thr Thr Pro Thr Pro Val
210 215 220

Thr Ala Thr Ser Ala Ser Glu Leu Glu Ala Glu His Phe Thr Phe Pro
225 230 235 240

Trp Leu Glu Asn Gly Val Asp His Tyr Glu Pro Thr Pro Ala Asn Glu
245 250 255

Asn Ser Asn Val Thr Val Arg Leu Gly Thr Met Ser Pro Thr Leu Ile
260 265 270

Gly Val Thr Val Ala Ala Val Val Ser Ala Thr Ile Gly Leu Val Ile
275 280 285

Val Ile Ser Ile Val Thr Arg Asn Met Cys Thr Pro His Arg Lys Leu
290 295 300

Asp Thr Val Ser Gln Asp Asp Glu Glu Arg Ser Gln Thr Arg Arg Glu
305 310 315 320

Ser Arg Lys Phe Gly Pro Met Val Ala Cys Glu Ile Asn Lys Gly Ala
325 330 335

Asp Gln Asp Ser Glu Leu Val Glu Leu Val Ala Ile Val Asn Pro Ser
340 345 350

Ala Leu Ser Ser Pro Asp Ser Ile Lys Met
355 360

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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Met Asn Met Leu Val Ile Val Leu Ala Ser Cys Leu Ala Arg Leu Thr
 1             5             10             15
Phe Ala Thr Arg His Val Leu Phe Leu Glu Gly Thr Gln Ala Val Leu
          20             25             30
Gly Glu Asp Asp Pro Arg Asn Val Pro Glu Gly Thr Val Ile Lys Trp
          35             40             45
Thr Lys Val Leu Arg Asn Ala Cys Lys Met Lys Ala Ala Asp Val Cys
          50             55             60
Ser Ser Pro Asn Tyr Cys Phe His Asp Leu Ile Tyr Asp Gly Gly Lys
          65             70             75             80
Lys Asp Cys Pro Pro Ala Gly Pro Leu Ser Ala Asn Leu Val Ile Leu
          85             90             95
Leu Lys Arg Gly Glu Ser Phe Val Val Leu Gly Ser Gly Leu His Asn
          100            105            110
Ser Asn Ile Thr Asn Ile Met Trp Thr Glu Tyr Gly Gly Leu Leu Phe
          115            120            125
Asp Pro Val Thr Arg Ser Asp Glu Gly Ile Tyr Phe Arg Arg Ile Ser
          130            135            140
Gln Pro Asp Leu Ala Met Glu Thr Thr Ser Tyr Asn Val Ser Val Leu
          145            150            155            160
Ser His Val Asp Glu Lys Ala Pro Ala Pro His Glu Val Glu Ile Asp
          165            170            175
Thr Ile Lys Pro Ser Glu Ala His Ala His Val Glu Leu Gln Met Leu
          180            185            190
Pro Phe His Glu Leu Asn Asp Asn Ser Pro Thr Tyr Val Thr Pro Val
          195            200            205
Leu Arg Val Phe Pro Pro Thr Glu His Val Lys Phe Asn Val Thr Tyr
          210            215            220
Ser Trp Tyr Gly Phe Asp Val Lys Glu Glu Cys Glu Glu Val Lys Leu
          225            230            235            240
Phe Glu Pro Cys Val Tyr His Pro Thr Asp Gly Lys Cys Gln Phe Pro
          245            250            255
Ala Thr Asn Gln Arg Cys Leu Ile Gly Ser Val Leu Met Ala Glu Phe
          260            265            270
Leu Gly Ala Ala Ser Leu Leu Asp Cys Ser Arg Asp Thr Leu Glu Asp
          275            280            285
Cys His Glu Asn Arg Val Pro Asn Leu Arg Phe Asp Ser Arg Leu Ser
          290            295            300

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Glu Ser Arg Ala Gly Leu Val Ile Ser Pro Leu Ile Ala Ile Pro Lys
305 310 315 320

Val Leu Ile Ile Val Val Ser Asp Gly Asp Ile Leu Gly Trp Ser Tyr
325 330 335

Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Glu Thr His
340 345 350

Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro Gly
355 360 365

Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala Gly
370 375 380

Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly Lys
385 390 395 400

Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu Pro
405 410 415

Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu Thr
420 425 430

Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe Arg
435 440 445

Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe Gly
450 455 460

Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile Ala
465 470 475 480

Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn Met
485 490 495

Asp Ser Tyr

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Phe Lys Thr Arg Gly Ala Glu Asp Ala Ala Ala Gly Lys Asn
1 5 10 15

Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile Leu Pro Thr Arg Leu Arg
20 25 30

Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser Asn Tyr Thr Gln Pro Ile
35 40 45

Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg Gly Glu Ser Asp Asn His
50 55 60

Ala Cys Lys Asp Thr Phe Tyr Arg Arg Thr Cys Cys Ala Ser Arg Ser
65 70 75 80

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Thr Val Ser Ser Gln Pro Asp Ser Pro His Thr Pro Met Pro Thr Glu
85 90 95

Tyr Gly Arg Val Pro Ser Ala Lys Arg Lys Lys Leu Ser Ser Ser Asp
100 105 110

Xaa Glu Gly Ala His Gln Pro Leu Val Ser Cys Lys Leu Pro Asp Ser
115 120 125

Gln Ala Ala Pro Ala Arg Thr Tyr Ser Ser Ala Gln Arg Tyr Thr Val
130 135 140

Asp Glu Val Ser Ser Pro Thr Pro Pro Gly Val Asp Ala Val Ala Asp
145 150 155 160

Leu Glu Thr Arg Ala Glu Leu Pro Gly Ala Thr Thr Glu Gln Thr Glu
165 170 175

Ser Lys Asn Lys Leu Pro Asn Gln Gln Ser Arg Leu Lys Pro Lys Pro
180 185 190

Thr Asn Glu His Val Gly Gly Glu Arg Cys Pro Ser Glu Gly Thr Val
195 200 205

Glu Ala Pro Ser Leu Gly Ile Leu Ser Arg Val Gly Ala Ala Ile Ala
210 215 220

Asn Glu Leu Ala Arg Met Arg Arg Ala Cys Leu Pro Leu Ala Ala Ser
225 230 235 240

Ala Ala Ala Ala Gly Ile Val Ala Trp Ala Ala Ala Arg Ala Leu Gln
245 250 255

Lys Gln Gly Arg
260

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG CAC CGT CCT CAT CTC AGA CGG CAC TCG CGT TAC TAC GCG AAA GGA	48
Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly	
1 5 10 15	
GAG GTG CTT AAC AAA CAC ATG GAT TGC GGT GGA AAA CGG TGC TGC TCA	96
Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Cys Ser	
20 25 30	

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GGC GCA GCT GTA TTC ACT CTT TTC TGG ACT TGT GTC AGG ATT ATG CGG Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg 35 40 45	144
GAG CAT ATC TGC TTT GTA CGC AAC GCT ATG GAC CGC CAT TTA TTT TTG Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu 50 55 60	192
AGG AAT GCT TTT TGG ACT ATC GTA CTG CTT TCT TCC TTC GCT AGC CAG Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln 65 70 75 80	240
AGC ACC GCC GCC GTC ACG TAC GAC TAC ATT TTA GGC CGT CGC GCG CTC Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu 85 90 95	288
GAC GCG CTA ACC ATA CCG GCG GTT GGC CCG TAT AAC AGA TAC CTC ACT Asp Ala Leu Thr Ile Pro Ala Val Gly Pro Tyr Asn Arg Tyr Leu Thr 100 105 110	336
AGG GTA TCA AGA GGC TGC GAC GTT GTC GAG CTC AAC CCG ATT TCT AAC Arg Val Ser Arg Gly Cys Asp Val Val Glu Leu Asn Pro Ile Ser Asn 115 120 125	384
GTG GAC GAC ATG ATA TCG GCG GCC AAA GAA AAA GAG AAG GGG GGC CCT Val Asp Asp Met Ile Ser Ala Ala Lys Glu Lys Glu Lys Gly Gly Pro 130 135 140	432
TTC GAG GCC TCC GTC GTC TGG TTC TAC GTG ATT AAG GGC GAC GAC GGC Phe Glu Ala Ser Val Val Trp Phe Tyr Val Ile Lys Gly Asp Asp Gly 145 150 155 160	480
GAG GAC AAG TAC TGT CCA ATC TAT AGA AAA GAG TAC AGG GAA TGT GGC Glu Asp Lys Tyr Cys Pro Ile Tyr Arg Lys Glu Tyr Arg Glu Cys Gly 165 170 175	528
GAC GTA CAA CTG CTA TCT GAA TGC GCC GTT CAA TCT GCA CAG ATG TGG Asp Val Gln Leu Leu Ser Glu Cys Ala Val Gln Ser Ala Gln Met Trp 180 185 190	576
GCA GTG GAC TAT GTT CCT AGC ACC CTT GTA TCG CGA AAT GGC GCG GGA Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly 195 200 205	624
CTG ACT ATA TTC TCC CCC ACT GCT GCG CTC TCT GGC CAA TAC TTG CTG Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu 210 215 220	672
ACC CTG AAA ATC GGG AGA TTT GCG CAA ACA GCT CTC GTA ACT CTA GAA Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu 225 230 235 240	720
GTT AAC GAT CGC TGT TTA AAG ATC GGG TCG CAG CTT AAC TTT TTA CCG Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro 245 250 255	768
TCG AAA TGC TGG ACA ACA GAA CAG TAT CAG ACT GGA TTT CAA GGC GAA Ser Lys Cys Trp Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu 260 265 270	816
CAC CTT TAT CCG ATC GCA GAC ACC AAT ACA CGA CAC GCG GAC GAC GTA His Leu Tyr Pro Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val 275 280 285	864
TAT CCG GGA TAC GAA GAT ATT CTG CAG CGC TGG AAT AAT TTG CTG AGG Tyr Arg Gly Tyr Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg 290 295 300	912

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AAA AAG AAT CCT AGC GCG CCA GAC CCT CGT CCA GAT AGC GTC CCG CAA	960
Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln	
305 310 315 320	
GAA ATT CCC GCT GTA ACC AAG AAA GCG GAA GGG CGC ACC CCG GAC GCA	1008
Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala	
325 330 335	
GAA AGC AGC GAA AAG AAG GCC CCT CCA GAA GAC TCG GAG GAC GAC ATG	1056
Glu Ser Ser Glu Lys Lys Ala Pro Glu Glu Asp Ser Glu Asp Asp Met	
340 345 350	
CAG GCA GAG GCT TCT GGA GAA AAT CCT GCC GCC CTC CCC GAA GAC GAC	1104
Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp	
355 360 365	
GAA GTC CCC GAG GAC ACC GAG CAC GAT GAT CCA AAC TCG GAT CCT GAC	1152
Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp	
370 375 380	
TAT TAC AAT GAC ATG CCC GCC GTG ATC CCG GTG GAG GAG ACT ACT AAA	1200
Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys	
385 390 395 400	
AGT TCT AAT GCC GTC TCC ATG CCC ATA TTC GCG GCG TTC GTA GCC TGC	1248
Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys	
405 410 415	
GCG GTC GCG CTC GTG GGG CTA CTG GTT TGG AGC ATC GTA AAA TGC GCG	1296
Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala	
420 425 430	
CGT AGC TAA	1305
Arg Ser	
435	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly	
1 5 10 15	
Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Ser	
20 25 30	
Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg	
35 40 45	
Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu	
50 55 60	
Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln	
65 70 75 80	
Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu	
85 90 95	

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Asp Ala Leu Thr Ile Pro Ala Val Gly Pro Tyr Asn Arg Tyr Leu Thr
 100 105 110
 Arg Val Ser Arg Gly Cys Asp Val Val Glu Leu Asn Pro Ile Ser Asn
 115 120 125
 Val Asp Asp Met Ile Ser Ala Ala Lys Glu Lys Glu Lys Gly Gly Pro
 130 135 140
 Phe Glu Ala Ser Val Val Trp Phe Tyr Val Ile Lys Gly Asp Asp Gly
 145 150 155 160
 Glu Asp Lys Tyr Cys Pro Ile Tyr Arg Lys Glu Tyr Arg Glu Cys Gly
 165 170 175
 Asp Val Gln Leu Leu Ser Glu Cys Ala Val Gln Ser Ala Gln Met Trp
 180 185 190
 Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly
 195 200 205
 Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu
 210 215 220
 Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu
 225 230 235 240
 Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro
 245 250 255
 Ser Lys Cys Trp Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu
 260 265 270
 His Leu Tyr Pro Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val
 275 280 285
 Tyr Arg Gly Tyr Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg
 290 295 300
 Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln
 305 310 315 320
 Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala
 325 330 335
 Glu Ser Ser Glu Lys Lys Ala Pro Glu Asp Ser Glu Asp Asp Met
 340 345 350
 Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp
 355 360 365
 Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp
 370 375 380
 Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys
 385 390 395 400
 Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys
 405 410 415
 Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala
 420 425 430
 Arg Ser

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(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 690 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GCG CCT GTA AAA GTG ACT ATA GTT TCT GCG GTC GAT TCG CAC TAC	48
Met Ala Pro Val Lys Val Thr Ile Val Ser Ala Val Asp Ser His Tyr	
1 5 10 15	
AAA CTA CCT AAT TCT AGA TTT GAG CTC TCG GAT TCT GGA TGG AAA GAA	96
Lys Leu Pro Asn Ser Arg Phe Glu Leu Ser Asp Ser Gly Trp Lys Glu	
20 25 30	
TTG GTT CAC GCA GTG AAA ACT ATG GCG AGT TAC GAT CGT CCG AGT ACA	144
Leu Val His Ala Val Lys Thr Met Ala Ser Tyr Asp Arg Pro Ser Thr	
35 40 45	
TTA TCG GTA ATC GTG CGC CCG GCA TCT CTG TAC GAA GTT TCC GGG GAG	192
Leu Ser Val Ile Val Arg Pro Ala Ser Leu Tyr Glu Val Ser Gly Glu	
50 55 60	
CTG TTT TCC CTT CCC AGG ATG TGC AGA CCC GTG ATT CGG TTC GGT GAG	240
Leu Phe Ser Leu Pro Arg Met Cys Arg Pro Val Ile Arg Phe Gly Glu	
65 70 75 80	
GGG GGC GAC CCG CCT GGA GTA AGT CCC GAG TGG AGC GGC TTG GAC GCA	288
Gly Gly Asp Pro Pro Gly Val Ser Pro Glu Trp Ser Gly Leu Asp Ala	
85 90 95	
GGG TTT TAC CAT TTG TCA TCT GGC GCG TAT GCC GCA AAA GAG TTC CAT	336
Gly Phe Tyr His Leu Ser Ser Gly Ala Tyr Ala Ala Lys Glu Phe His	
100 105 110	
TTG TGG GTG CTG GGT ACC GCT GAC ATA TGC ATG GCA GCT TTA AAC CTC	384
Leu Trp Val Leu Gly Thr Ala Asp Ile Cys Met Ala Ala Leu Asn Leu	
115 120 125	
CCT GCG CCA AAA ACT TTC CTA ATT ACC GAA ACC GGA GGT AAA AAT TTT	432
Pro Ala Pro Lys Thr Phe Leu Ile Thr Glu Thr Gly Gly Lys Asn Phe	
130 135 140	
GAG AGA GGA GTG GAA ATA TTT TTG GTA AAC GGA GAC AAG ACA ACG CTG	480
Glu Arg Gly Val Glu Ile Phe Leu Val Asn Gly Asp Lys Thr Thr Leu	
145 150 155 160	
TCT CTG AGT CAC CCA TCA GTC TGG ACA ACT CTT GCC CCT TCG AGC CTG	528
Ser Leu Ser His Pro Ser Val Trp Thr Thr Leu Ala Pro Ser Ser Leu	
165 170 175	

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AGA ACG CCC TGG CCG TAC AGC ACG GTA AAG TTT TTA AAA GTA AAA CCT	576
Arg Thr Pro Trp Pro Tyr Ser Thr Val Lys Phe Leu Lys Val Lys Pro	
180 185 190	
AAC TCG GCC GCA TAC TGT GTT TCC GAC TCG GAT GAT GGC GAA CGG CAG	624
Asn Ser Ala Ala Tyr Cys Val Ser Asp Ser Asp Asp Gly Glu Arg Gln	
195 200 205	
CCA AAA TTT TTT CTC GGG AGT CTA TTT AAG TCG AAG AAA CCC CGC TCC	672
Pro Lys Phe Phe Leu Gly Ser Leu Phe Lys Ser Lys Lys Pro Arg Ser	
210 215 220	
CCG CGG CGC CGA CGT TA G	690
Pro Arg Arg Arg Arg	
225	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Ala Pro Val Lys Val Thr Ile Val Ser Ala Val Asp Ser His Tyr	
1 5 10 15	
Lys Leu Pro Asn Ser Arg Phe Glu Leu Ser Asp Ser Gly Trp Lys Glu	
20 25 30	
Leu Val His Ala Val Lys Thr Met Ala Ser Tyr Asp Arg Pro Ser Thr	
35 40 45	
Leu Ser Val Ile Val Arg Pro Ala Ser Leu Tyr Glu Val Ser Gly Glu	
50 55 60	
Leu Phe Ser Leu Pro Arg Met Cys Arg Pro Val Ile Arg Phe Gly Glu	
65 70 75 80	
Gly Gly Asp Pro Pro Gly Val Ser Pro Glu Trp Ser Gly Leu Asp Ala	
85 90 95	
Gly Phe Tyr His Leu Ser Ser Gly Ala Tyr Ala Ala Lys Glu Phe His	
100 105 110	
Leu Trp Val Leu Gly Thr Ala Asp Ile Cys Met Ala Ala Leu Asn Leu	
115 120 125	
Pro Ala Pro Lys Thr Phe Leu Ile Thr Glu Thr Gly Gly Lys Asn Phe	
130 135 140	
Glu Arg Gly Val Glu Ile Phe Leu Val Asn Gly Asp Lys Thr Thr Leu	
145 150 155 160	
Ser Leu Ser His Pro Ser Val Trp Thr Thr Leu Ala Pro Ser Ser Leu	
165 170 175	
Arg Thr Pro Trp Pro Tyr Ser Thr Val Lys Phe Leu Lys Val Lys Pro	
180 185 190	
Asn Ser Ala Ala Tyr Cys Val Ser Asp Ser Asp Asp Gly Glu Arg Gln	
195 200 205	

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Pro Lys Phe Phe Leu Gly Ser Leu Phe Lys Ser Lys Lys Pro Arg Ser
210 215 220

Pro Arg Arg Arg Arg
225

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG CGT AGC TCA GTT ACG TCA TTG TGG AGC CCT TCA GAT CAC GCC TCT	48
Met Arg Ser Ser Val Thr Ser Leu Trp Ser Pro Ser Asp His Ala Ser	
1 5 10 15	
TCG CCC GCA AAT GCC AAG CAT TTT TAT CAT ATT TCC GAT TTC CGG CGC	96
Ser Pro Ala Asn Ala Lys His Phe Tyr His Ile Ser Asp Phe Arg Arg	
20 25 30	
GCG GAA ACG GCG CCT GCG GGC GGT ACG GGC GCG CGA ACT GAG GTT AAG	144
Ala Glu Thr Ala Pro Ala Gly Thr Gly Ala Arg Thr Glu Val Lys	
35 40 45	
CGT CGC GCT TTC ACT TTC CCA GCG GCA GCG GTA CTC AGC GCA ACT GAA	192
Arg Arg Ala Phe Thr Phe Pro Ala Ala Val Leu Ser Ala Thr Glu	
50 55 60	
GCC CGA ACC GGC TCG TCT ATC ACC GGC TTA AAC CGT ACT CCG TCT GCA	240
Ala Arg Thr Gly Ser Ser Ile Thr Gly Leu Asn Arg Thr Pro Ser Ala	
65 70 75 80	
ATA ATT TCC CTT GCA TGG TCC GAA ATG AGA AAT CTT AAG GAC CCC CTC	288
Ile Ile Ser Leu Ala Trp Ser Glu Met Arg Asn Leu Lys Asp Pro Leu	
85 90 95	
GGG TCC CTG TCG CTG GAA ATA GCT TTA ACG AAT GTC TCT AAC TTT TCC	336
Gly Ser Leu Ser Leu Glu Ile Ala Leu Thr Asn Val Ser Asn Phe Ser	
100 105 110	
CTC TTG AGC TCA GAC CCC ATG GCC TTC GAA AAG TCT TCA TAT TG	380
Leu Leu Ser Ser Asp Pro Met Ala Phe Glu Lys Ser Ser Tyr	
115 120 125	
A	381

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Met Arg Ser Ser Val Thr Ser Leu Trp Ser Pro Ser Asp His Ala Ser
 1           5           10           15
Ser Pro Ala Asn Ala Lys His Phe Tyr His Ile Ser Asp Phe Arg Arg
          20           25           30
Ala Glu Thr Ala Pro Ala Gly Gly Thr Gly Ala Arg Thr Glu Val Lys
          35           40           45
Arg Arg Ala Phe Thr Phe Pro Ala Ala Ala Val Leu Ser Ala Thr Glu
          50           55           60
Ala Arg Thr Gly Ser Ser Ile Thr Gly Leu Asn Arg Thr Pro Ser Ala
          65           70           75           80
Ile Ile Ser Leu Ala Trp Ser Glu Met Arg Asn Leu Lys Asp Pro Leu
          85           90           95
Gly Ser Leu Ser Leu Glu Ile Ala Leu Thr Asn Val Ser Asn Phe Ser
          100          105          110
Leu Leu Ser Ser Asp Pro Met Ala Phe Glu Lys Ser Ser Tyr
          115          120          125

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

ATG TGG TGT CGT TTG CAC TGG ATA AGT CCT CGG TTC AGT ATT ATG CGT      48
Met Trp Cys Arg Leu His Trp Ile Ser Pro Arg Phe Ser Ile Met Arg
 1           5           10           15
CCC GGT TCC CGA ACT GGT AGG GTT TTG CGA GGC CAG GGG TGT GCT CTG      96
Pro Gly Ser Arg Thr Gly Arg Val Leu Arg Gly Gln Gly Cys Ala Leu
          20           25           30
TGC AGT TTC TGG CAT CGT ACT CGA ACT CCG AGT ATA AAC CTC CGG TGC      144
Cys Ser Phe Trp His Arg Thr Arg Thr Pro Ser Ile Asn Leu Arg Cys
          35           40           45

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CGC GCT CGG GGT CTG AGT AAT TTC CGG CTC TGC GCC CAG AGT CCG GGT Arg Ala Arg Gly Leu Ser Asn Phe Arg Leu Cys Ala Gln Ser Pro Gly 50 55 60	192
GAA AGG CAC AGG TTC GGT ACT CGG ACT CTG AGT CAA CAC CTC CCG CTC Glu Arg His Arg Phe Gly Thr Arg Thr Leu Ser Gln His Leu Arg Leu 65 70 75 80	240
TGT ACT CGG AGT CTG AGT AGC TTT CGG TAC CGT ACT CCG GGC CTG AGT Cys Thr Arg Ser Leu Ser Ser Phe Arg Tyr Arg Thr Arg Gly Leu Ser 85 90 95	288
GAA AAA GTG TGT TTC AGT ACT CTG AGT TCG CAT AGT GTC CCG CTC GGC Glu Lys Val Cys Phe Ser Thr Leu Ser Ser His Ser Val Arg Leu Gly 100 105 110	336
ACT CGA AGT CTG AGT AAA GGC CTC AGT TCC CGC GCT CTG AGT CCG AGT Thr Arg Ser Leu Ser Lys Gly Leu Ser Ser Arg Ala Leu Ser Pro Ser 115 120 125	384
AAA AAT CGC CGG TTC AGT ACT CGA ACT CAG AGT AGT TTT CCG TAC CGT Lys Asn Arg Arg Phe Ser Thr Arg Thr Gln Ser Ser Phe Arg Tyr Arg 130 135 140	432
GCT CGG GGT CTG AGT AAA CAC CTC CGT TAC CGT ACT CGA ACT CTG TGT Ala Arg Gly Leu Ser Lys His Leu Arg Tyr Arg Thr Arg Thr Leu Cys 145 150 155 160	480
AAA AAC CTC CGG CGC CGC GCT CGG AGC GCG AGC GGT TTC GGG GGG CGT Lys Asn Leu Arg Arg Ala Arg Ser Ala Ser Gly Phe Gly Gly Arg 165 170 175	528
GCT ACG AGA CTG AGT AAA TAT CTC GGG TAT CGT GCT CCG GGT CTG GGC Ala Thr Arg Leu Ser Lys Tyr Leu Gly Tyr Arg Ala Arg Gly Leu Gly 180 185 190	576
AGG TGC CTC GGT TTC TGC ACC CGG AGT CTG AGT AAA AGT CAT CTG TTC Arg Cys Leu Gly Phe Cys Thr Arg Ser Leu Ser Lys Ser His Leu Phe 195 200 205	624
AGC ACT CGG AGT CTG AGT AAA CAA CGC CTC CGT TTC TGC GAT CTG CGT Ser Thr Arg Ser Leu Ser Lys Gln Arg Leu Arg Phe Cys Asp Leu Arg 210 215 220	672
CTG AGT AAG AGC CGC CTG TTC AGT ACT CGG AGT CTG AGT AAA ATA CCA Leu Ser Lys Ser Arg Leu Phe Ser Thr Arg Ser Leu Ser Lys Ile Pro 225 230 235 240	720
CGG TTC CTG ACT CTG GGA CCG CGC GGT TTC CGA CTC GGT ACT CCG ACT Arg Phe Leu Thr Leu Gly Pro Arg Gly Phe Arg Leu Gly Thr Arg Thr 245 250 255	768
CTG AGT AAA GAC CAC CGT TTC TGC ACT CTG GGT CTG TGT AGT TTC ATG Leu Ser Lys Asp His Arg Phe Cys Thr Leu Gly Leu Cys Ser Phe Met 260 265 270	816
TGC CGC GCT CGG GGT CTC GGT AGA AAT CCC CGG CGC GGT CGT AGG AAA Cys Arg Ala Arg Gly Leu Gly Arg Asn Pro Arg Arg Gly Arg Arg Lys 275 280 285	864
CAG TGT ATT TTC TG A Gln Cys Ile Phe 290	879

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Met Trp Cys Arg Leu His Trp Ile Ser Pro Arg Phe Ser Ile Met Arg
 1          5          10          15
Pro Gly Ser Arg Thr Gly Arg Val Leu Arg Gly Gln Gly Cys Ala Leu
          20          25          30
Cys Ser Phe Trp His Arg Thr Arg Thr Pro Ser Ile Asn Leu Arg Cys
          35          40          45
Arg Ala Arg Gly Leu Ser Asn Phe Arg Leu Cys Ala Gln Ser Pro Gly
          50          55          60
Glu Arg His Arg Phe Gly Thr Arg Thr Leu Ser Gln His Leu Arg Leu
          65          70          75          80
Cys Thr Arg Ser Leu Ser Ser Phe Arg Tyr Arg Thr Arg Gly Leu Ser
          85          90          95
Glu Lys Val Cys Phe Ser Thr Leu Ser Ser His Ser Val Arg Leu Gly
          100          105          110
Thr Arg Ser Leu Ser Lys Gly Leu Ser Ser Arg Ala Leu Ser Pro Ser
          115          120          125
Lys Asn Arg Arg Phe Ser Thr Arg Thr Gln Ser Ser Phe Arg Tyr Arg
          130          135          140
Ala Arg Gly Leu Ser Lys His Leu Arg Tyr Arg Thr Arg Thr Leu Cys
          145          150          155          160
Lys Asn Leu Arg Arg Arg Ala Arg Ser Ala Ser Gly Phe Gly Gly Arg
          165          170          175
Ala Thr Arg Leu Ser Lys Tyr Leu Gly Tyr Arg Ala Arg Gly Leu Gly
          180          185          190
Arg Cys Leu Gly Phe Cys Thr Arg Ser Leu Ser Lys Ser His Leu Phe
          195          200          205
Ser Thr Arg Ser Leu Ser Lys Gln Arg Leu Arg Phe Cys Asp Leu Arg
          210          215          220
Leu Ser Lys Ser Arg Leu Phe Ser Thr Arg Ser Leu Ser Lys Ile Pro
          225          230          235          240
Arg Phe Leu Thr Leu Gly Pro Arg Gly Phe Arg Leu Gly Thr Arg Thr
          245          250          255
Leu Ser Lys Asp His Arg Phe Cys Thr Leu Gly Leu Cys Ser Phe Met
          260          265          270
Cys Arg Ala Arg Gly Leu Gly Arg Asn Pro Arg Arg Gly Arg Arg Lys
          275          280          285
Gln Cys Ile Phe
          290
  
```

(2) INFORMATION FOR SEQ ID NO:18:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 534 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..533
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG CTC CCA AGC CTA CTC AAC AGG GGC TCT CCC CGG CTG AAT TCT CCT	48
Met Leu Pro Ser Leu Leu Asn Arg Gly Ser Pro Arg Leu Asn Ser Pro	
1 5 10 15	
CCT AAG TGT TCA GAG GCC TCT GCT GTA CCA TAT AAC TAT CGT GTA GTA	96
Pro Lys Cys Ser Glu Ala Ser Ala Val Pro Tyr Asn Tyr Arg Val Val	
20 25 30	
CGC CCC TCC CAG TCC GTG TCC GAT ACT GCC CCT TTT GAG AGG ATT GGG	144
Arg Pro Ser Gln Ser Val Ser Asp Thr Ala Pro Phe Glu Arg Ile Gly	
35 40 45	
AGA TTA GAG AAT CGA AAT GAT TGG AGA GCC ACA TTC AGA CTT AAT CAC	192
Arg Leu Glu Asn Arg Asn Asp Trp Arg Ala Thr Phe Arg Leu Asn His	
50 55 60	
ATT TTT ATT GAG TCG GGC GAG CTT AGC GCA GAC GGG TTA ACA ATC GCA	240
Ile Phe Ile Glu Ser Gly Glu Leu Ser Ala Asp Gly Leu Thr Ile Ala	
65 70 75 80	
ACC AGT TCC ACA AGT TCA CTA TCC TGG TCA GCG CCC TTG TTT ATT TCG	288
Thr Ser Ser Thr Ser Ser Leu Ser Trp Ser Ala Pro Leu Phe Ile Ser	
85 90 95	
CAC GCA ACC ATG GGT CCA AAT TTT CGC GAT TCC CTT CTA GTT TGG GAA	336
His Ala Thr Met Gly Pro Asn Phe Arg Asp Ser Leu Leu Val Trp Glu	
100 105 110	
CGT TCT TCG TCG TCT TGC GAG ACC GTG TCT AAT TTT CGG TGC GGG GTG	384
Arg Ser Ser Ser Ser Cys Glu Thr Val Ser Asn Phe Arg Cys Gly Val	
115 120 125	
CAC ATG TTT CTG GTG ACG ATG GAA ATT ACA ATG ACG AGG CCG ATC GTT	432
His Met Phe Leu Val Thr Met Glu Ile Thr Met Thr Arg Pro Ile Val	
130 135 140	
GCG CTC ACG ACG GCA GCC ACG GTT ACC CCA ATT AGC GTA GGG CTC ATT	480
Ala Leu Thr Thr Ala Ala Thr Val Thr Pro Ile Ser Val Gly Leu Ile	
145 150 155 160	
GTC CCG AGA CGG ACA GTA ACG TTT GAA TTT TCG TTT GCG GGT GTC GGT	528
Val Pro Arg Arg Thr Val Thr Phe Glu Phe Ser Phe Ala Gly Val Gly	
165 170 175	
TCG TA A	534
Ser	

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(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Leu Pro Ser Leu Leu Asn Arg Gly Ser Pro Arg Leu Asn Ser Pro
 1 5 10 15
 Pro Lys Cys Ser Glu Ala Ser Ala Val Pro Tyr Asn Tyr Arg Val Val
 20 25 30
 Arg Pro Ser Gln Ser Val Ser Asp Thr Ala Pro Phe Glu Arg Ile Gly
 35 40 45
 Arg Leu Glu Asn Arg Asn Asp Trp Arg Ala Thr Phe Arg Leu Asn His
 50 55 60
 Ile Phe Ile Glu Ser Gly Glu Leu Ser Ala Asp Gly Leu Thr Ile Ala
 65 70 75 80
 Thr Ser Ser Thr Ser Ser Leu Ser Trp Ser Ala Pro Leu Phe Ile Ser
 85 90 95
 His Ala Thr Met Gly Pro Asn Phe Arg Asp Ser Leu Leu Val Trp Glu
 100 105 110
 Arg Ser Ser Ser Ser Cys Glu Thr Val Ser Asn Phe Arg Cys Gly Val
 115 120 125
 His Met Phe Leu Val Thr Met Glu Ile Thr Met Thr Arg Pro Ile Val
 130 135 140
 Ala Leu Thr Thr Ala Ala Thr Val Thr Pro Ile Ser Val Gly Leu Ile
 145 150 155 160
 Val Pro Arg Arg Thr Val Thr Phe Glu Phe Ser Phe Ala Gly Val Gly
 165 170 175
 Ser

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATTCGAGC TCGGTACCCG GATAATACGT ACATGTTAAC GCAGAGGT

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(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCTGACCCT AGTCGACCTG CAGTGAATAA TAAAAT

36

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTCCGTCGA GATCCTCTAG AGTCGACGAA AGGTCAGAGA CGATGCCC

48

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGATCAGAA ACTCTTTTCG TACCCGGGAT CCTCTAGA

38

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATACAAGC TTAGATGCAT ATTACTCGA GCC

33

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTTGGCGG AGCGGATATG ATCTCGACCT GCAGTGAATA ATAAATGTG T

51

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGTCCTCGA GATCCTCTAG AGTCGAGATC AGCAAAATGT TCACGGGG

48

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

09993777-440604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAGCTTGGCG TAATCATG

18

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGAATTCGAG CTCGGTACCT CGTGGCGAGC GCAGGCGGC

39

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCCGAGTTA GGTTTTACTT TTCTAGAGGA TCCCTCGAC GTCTGGGCGC

51

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGCTGCGTT CCCGGGATC CTCTAGAATT AGGTAGTTTG TAGTGCGA

48

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCAAGATCCA GGAAATCCTT CGGTACCGAG CTCGAATTCG TA

42

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GAATTCGAGC TCGGTACCGA AAGCTACTCA GAC

33

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGCAACAGC TCTCGTAACT CTAGAAGTTA ACGATCGCTG TT

42

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GAATAGCATA CCAATGCCTA TTCATTGGGA CTCGACTCTA GAGGATCCCC GGGAACG

57

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCGAGGGGAT CCTCTAGAGT CGAGGGACCC ATGGTTGCGT GC

42

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTTACTAAAG CGCGCGGAAA GCTTCGTCGT GCTGGGTTCT GG

42

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGCTTGGCG TAATCATGCT C

21

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGAATTGCAG CTCGGTACCC GGATAATACG TACATGTITAA CGCAGAGG

48

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATCTATTGGA GCGTTTAGCG CGCGTCGACG AAAGGTCAGA GACGA

45

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGCCTCAT TCTGATCCCC GGGAAACG

27

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:

0999377.110601

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCACCCCG CGCCCCGAC GTCGAGGGA TCAATTATTG CGTATTGAAT A

51

- (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATCAGAAACT CTTTCGGTAC CGAGCTCGAA TTC

33

- (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAATTCGAGC TCGGTACCCG GATAATACGT ACATGTTAAC GCAGAGGT

48

- (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCTGACCGCT AGTCGACTCT AGAGGATCCC CTC

33

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGTCCCGGG GATCCTCTAG AGTCGACGGC AGAGTCGCAG AC

42

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGATCCAAAC TCGGATCCTC TAGAGTCGAC

30

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

00993777.110601

AAGCTTGGGC TGCAGGTGCA CTCTAGAGGA TCCCCTCGAC GTCTGGGG

48

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CACACCTTTG CGCATCTCCA CAGCTCAACA ATGAATTCCA TGTTACGTCC TGTAGAAACC

60

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGGAGGCA AACAAATGAAT CAACAACTCT CCCGGGAGAT GGGGGAGGCT AACTGAAACA

60

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGTCGCGTTC CCGGGGATCC TCTAGAGTCG ACCTGCAGCC CAAGC

45

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:

09993777.110601

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TCTAGAGTCG ACCTGCAGTG AATAATAAAA TGTGTGTTTG TCCGAAAT

48

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTCCATAGAA GACACCGGGA CCATGGATCC CGTCGTTTTA CAACG

45

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCGGCGGAAA TCCAGCTGAG CGCGGTCGC TACCATTACC AGTTGGTCTG GTGTCAAAAA
GATCTAGAAT AAGCTAGAGG ATCGATCCCC TATGGCGATC ATCAG

60

105

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCGTCGAGAT CCTCTAGAGT CGACCTGCAG GTCGAC

36

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CCTAGCACCC TTGTATCGCG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGCCTCGAGT CCAATGAAT AGGCATTGG

29

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:
CGCCTCGAGG ACCCATGGTT GCGTGCG

27

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTCGTCCGAA CGAGTTACG

20

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18912 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 697..1533
(D) OTHER INFORMATION:

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: complement (1900..2784)
(D) OTHER INFORMATION:

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: complement (2916..3605)
(D) OTHER INFORMATION:

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3694..5124
(D) OTHER INFORMATION:

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 5210..7081
(D) OTHER INFORMATION:

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 7245..8123
(D) OTHER INFORMATION:

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 8333..11290
(D) OTHER INFORMATION:

- (ix) FEATURE:
(A) NAME/KEY: CDS

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- (B) LOCATION: 11098..12402
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 12510..13598
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 13792..15291
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 15298..16080
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 16129..17013
(D) OTHER INFORMATION:
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: complement (17380..18216)
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGATCCCGAA GAGCTCTCCC AGAAGTTTT CTTCGCGAG GTATCGGAGG ACGAAGAACC	60
GGCACGCGGG AGGAGCTGGA GCGACCCGGA GTCGGAGGAA GAGCAGCCTG GGTGCCGGGG	120
AGTGSACTTG GCGGAGGAGG ACACGGGACA CAGCTCCACC GAGTCAGAGC CCACGCAATC	180
TGACTTAGAC TTATTAGACG ACAGCTCTCC GCGCGCGCCG CCATTGTGTA TCCCCCGCGT	240
CCGTGCGTTA TTGCGGTGCG CGGCACCCGC AAAGACCCAC GGAAGGCTTC GGCGCCAGS	300
GCGGGTAGGC GCACCTTTAA AAGACGGAGG TTGTCATTTT CTTCCTTCCT TGACGAGGAA	360
TCCGAGGAGA GAAGTAAAAA AGAAGAAGCG GCCTCGACCC CTGCACGGCG ACGCAAGGCC	420
GAGGCTTCGA CGAGCAGATA GAGGAGACGC GGGGCAGAAC CTCCCCCTCC TCCCCACCCC	480
CCTACTCTGG ACATTTATTG CCGGCTCGAT CCATTTCGAT CCAGAACTTC TTCCCGCTC	540
AGCCTTCACG CAGAAGCGGA CGCGCGCCCC TTTCGACCG CCGGACATCG CGCGCGCCCC	600
CCCCCTTCAC GCCCGGCGCA ATCCGTAGCC GTCCAAC TCGCAGCACA ACCGCAGTAG	660
ACCGCCCGGA CCGCTCTCCT CTAGACACAT CCTTAA ATG GAA AAC ATG CTC GAC	714
Met Glu Asn Met Leu Asp	
1 5	
GGG TGC TAC CCG CTG GCG CTG ATG GAC AGC GAT CAC ATT ACT GCG CAC	762
Gly Cys Tyr Pro Leu Ala Leu Met Asp Ser Asp His Ile Thr Ala His	
10 15 20	
GCG GTA CCT CGT GGC GAG CGC AGG CGG CAA GGT GCC GCT GTC GCC TCG	810
Ala Val Pro Arg Gly Glu Arg Arg Gln Gly Ala Val Ala Ser	
25 30 35	
TCG GAG TCG GCC GAC TCG GTA GAC CCG TGC ATT CGG ATC GCC TCG CGG	858
Ser Glu Ser Ala Asp Ser Val Asp Pro Cys Ile Arg Ile Ala Ser Arg	
40 45 50	
CTC TGG GCG GAG TTA GTC GAG ATA TCG TCC GAA CTC AAG GAC GGT TAC	906
Leu Trp Arg Glu Leu Val Glu Ile Ser Ser Glu Leu Lys Asp Gly Tyr	
55 60 65 70	

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GGA GAG TTC ACG TCA GCG AGA GAC CGC CGC AAC GCG CTG ATT GCT GCC Gly Glu Phe Thr Ser Ala Arg Asp Arg Arg Asn Ala Leu Ile Ala Ala 75 80 85	954
AAC GAA CGG CTA CGT TCG GCT TTT CTG GGG GCC AGC CGG GCG ACG CGC Asn Glu Arg Leu Arg Ser Ala Phe Leu Gly Ala Ser Arg Ala Thr Arg 90 95 100	1002
GGC CTA GGT TTG AGG CCG CGG TGG GCG TCG ACG GAG AGC GTC GCC AAC Gly Leu Gly Leu Arg Pro Arg Trp Ala Ser Thr Glu Ser Val Ala Asn 105 110 115	1050
TCC CCC ACT GAC CCG AAT AAC GGC AAC GGG TTG GGA GAA TTA GAG GAG Ser Pro Thr Asp Pro Asn Asn Gly Asn Gly Leu Gly Glu Leu Glu Glu 120 125 130	1098
GCA ATG GAA GGG ATC GAG GGC GAT TTC TGG CTC GAC TCT CTG GAC GGT Ala Met Glu Gly Ile Glu Gly Asp Phe Trp Leu Asp Ser Leu Asp Gly 135 140 145 150	1146
GAC CGC TTC GAG GAC GAG AGC CGT ACC ATG CAG AGC GAG AAT ATG CGT Asp Arg Phe Glu Asp Glu Ser Arg Thr Met Gln Ser Glu Asn Met Arg 155 160 165	1194
TTC GTG ATC GAG AAA GAA CTG TTA TCC TGG CTG TCC CGA CAC CTG CCG Phe Val Ile Glu Lys Glu Leu Leu Ser Trp Leu Ser Arg His Leu Pro 170 175 180	1242
GCC GAC CTC GCG TCC GCC GAG CGA GAG ACC TCC CGG TCT CTC CTG GCG Ala Asp Leu Ala Ser Ala Glu Arg Glu Thr Ser Arg Ser Leu Leu Ala 185 190 195	1290
GCC GGG CAC TGG TGC TGC TTG TGG CAC CCT CGG CCG TGC CGC GAA GCG Ala Gly His Trp Cys Cys Leu Trp His Pro Cys Arg Glu Ala 200 205 210	1338
TGT TTG TAC GAC TCG ATT TAC GTG CAG AGT CTT TTC TGC GTC GGG ACG Cys Leu Tyr Asp Ser Ile Tyr Val Gln Ser Leu Phe Cys Val Gly Thr 215 220 225 230	1386
GGG AGA GTC CCG CAA TCG GAG ATG CGC CGT CGC GAA TAC CTG GCC GCC Gly Arg Val Pro Gln Ser Glu Met Arg Arg Glu Gly Tyr Leu Ala Ala 235 240 245	1434
TTG CGC GCC GCG GCT GCC GCC AAC TCT CCC GAA GTG AGC GCC TCG Leu Arg Ala Gly Ala Ala Ala Ala Asn Ser Pro Glu Val Ser Ala Ser 250 255 260	1482
ATC TTT GCG AGG GAC GCT GGA ATC GCG CTG GCG CTG GCG CGC CGT Ile Phe Ala Arg Asp Ala Gly Ile Ala Leu Ala Leu Ala Arg Arg Arg 265 270 275	1530
TGA CGGGAGAATG ACGCCCTCTA GCGGCTTCT TACCTCCGCG TCCCTGACAA	1583
CCTCGCGGGT TTTTACACTG TCCTCCGTCC ACTCTCCCCC CTCACCCACT CCSCGGCAGC	1643
GAAACACAAAC CCCCCCCCCC CCCAGAAAC GAGCGACACG CGAGCGCTGC GAAATAAATA	1703
AAGTAATATT ATTGTGTGTT TTTACAGTTG TTGCAATCGA GAGGCCGTTT GTCTGTCTGT	1763
GTCTGTGCGG AGCTAGGCTT TCCCGGGCGG CCCGTTTCCA CCGTTCGGTT AGGCCGGTGG	1823
CGACGGGACA TAGAGAAGA TAGAGCGCGC GCCCTGGCGG CGAGAGGGTG TTGCGGGGGT	1883
AAATGGGACC CTGAGCTCAC CATTTTGGCG GGGGATTGCA CGGGAACAA AAGCTCTCT	1943

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CGCACATAAT GATTTCCTT AAACAGTGGC TGTAAAGCT TTCTCGACT GGGACGCGCA	2003
CGTCCGGAGA CATGATCTTA TCGGTAGCTA CACAGTTCAT GAGGTGGGCC ACGAACGCGC	2063
GGATCGAGTT TTGGGAACCT TCGGGAGGT CTTCGGGAG GGTGAAGTT GACAGAGGCA	2123
CGCTATAC CAGGAGGCTC CGCACCATCT CCATGCTAT CCTTATCGCC GCGAGTCCGG	2183
CGCGGGCGC GCTGCTCG TTATTCCAGT GCGCGGACCG CGAGTGCGCC CCTCCCCGGG	2243
CTCTGATATA GAGCACCAGC AGCTCGACGG CGGCGGAGAA AAAAGAAAGA ATGTCCGGCC	2303
CAATGACTGG AACTTTGGGC ACGTCTCTTA TTTCCACGC GCGCGCCCGG GGAATCTGCT	2363
TGCCCCAGAC CTTGCTTTCC AACTCCCCGT TCGGCCCCCC AACTAACTCC GACAGCGCGG	2423
TCCACAGTCC TACGCGCGT GCGACGCGC GCTTAGCCG GGGCGCTATT CCGGGTCTGT	2483
GCGCCGTGAT ATCTTCGGC ACCTGCAGAC TGCCACAGCT TTCCTCCCT TCAAAATACG	2543
CGCGGGCGC CTGTACGATC ACCGCGGCA GATCGGGCCA AAAGAAAAA TCGCAACTCT	2603
GCGACGCCC CCAGAAATCT CCTCCGGGCA GGTCCGTGCC CCTAAAGGCC GCCGAGAAAG	2663
CTAAGTCCAA ATGTGACGTC GGAGGTCTCG ACATGGTGC CAACCTCCA AATGCTACCC	2723
GCGGCCAC GCACGCGGG CTITTATAA GATGGCGCG GAGACAATA CACTTACTCA	2783
TCCGCTACG CGTTATTAT TGTCAATAT TGTGTGGTTA TTATTACTGC TACCGCCCTT	2843
GTTTCTGCAA GGCCCTCGCC GCGGCCAGG CCATATTCC GGCAGCGGCC GCCGACGCGG	2903
CGAGCTCGC CGCTAACGTC GCGCGCGCG GGAGCGGGT TTCTTCGACT TAAATAGACT	2963
CCCGAGAAAA AATTTTGGCT GCCGTTCCGC ATCATCCGAG TCGGAAACAC AGTATCGCGC	3023
CGAGTTAGT TTTACTTTTA AAAACTTTAC CGTGTGTAC GGCAGGGCG TTCTCAGGCT	3083
CGAAGGGCA AGAGTTGTCC AGACTGATG GTGACTCAGA GACAGCGTTG TCTTGTCTCC	3143
GTTTACCAAA AATATTTCCT CTCCTCTCT AAAATTTTTC CTCCGGTTT CGGTAATTAG	3203
GAAAGTTTT GCGCCAGGGA GGTTTAAAGC TGCCATGCAT ATGTACGCG TACCAGCAC	3263
CCACAAATGG AACTCTTTTG CGGCATACG GCCAGATGAC AAATGGTAAA ACCCTGCGTC	3323
CAAGCGCTC CACTCGGAC TTACTCCAG CGGCTCGCC CCTCACCGA ACCGAATCAC	3383
GGGTCTGCAC ATCTCGGAA GGGAAACAG CTCGCCGAA ACTTCGTACA GAGATCGCGG	3443
GCGCACGATT ACCGATAATG TACTCGGAC ATCGTAACT GCCATAGTTT TCACTGCGTG	3503
AACCAATTCT TTCCATCCAG AATCCGAGAG CTCAAATCTA GAATTAGGTA GTTTGTAGTG	3563
CGAATCGACC GCAGAACTA TAGTCACTT TACAGGCGCC ATCGCGCTCAG	3615
ACTCCACCCC GCTATGATGT CAGAAATATA ACGCTCTTAT TCTAGCAGAG TCAGGCCAAT	3675
ATATACAGCT TAGAGAAG ATG CGG TTT CGG CGC ATC TGT TCA CGC TCT AGG	3726
Met Arg Phe Arg Arg Ile Cys Ser Arg Ser Arg	
1 5 10	
GCA GAA AAA CGA AGA AGA ACA ACC GAG AAT CCG CTT ACC TCA AAA CGC	3774
Ala Glu Lys Arg Arg Thr Thr Glu Asn Pro Leu Thr Ser Lys Arg	
15 20 25	

GTT TGC GTA TTG GAT AGT TTC TCA CGG ACA ATG TCA TTG CGC CCC TAT Val Cys Val Leu Asp Ser Phe Ser Arg Thr Met Ser Leu Arg Pro Tyr 30 35 40	3822
GCA GAA ATT TTG CCG ACC GCG GAA GGC GTC GAG CGC CTC GCC GAA CTT Ala Glu Ile Leu Pro Thr Ala Glu Gly Val Glu Arg Leu Ala Glu Leu 45 50 55	3870
GTT AGT GTG ACA ATG ACA GAA GCG GCG GAA CCT GTG ACA GAG AAT ACA Val Ser Val Thr Met Thr Glu Arg Ala Glu Pro Val Thr Glu Asn Thr 60 65 70 75	3918
GCT GTA AAC AGT ATC CCC CCG GCT AAC GAG AAC GGG CAG AAC TTC GCA Ala Val Asn Ser Ile Pro Pro Ala Asn Glu Asn Gly Gln Asn Phe Ala 80 85 90	3966
TAT GCA GGC GAT GGG CCC TCG ACT ACT GAA AAA GTT GAC GGC TCG CAT Tyr Ala Gly Asp Gly Pro Ser Thr Thr Glu Lys Val Asp Gly Ser His 95 100 105	4014
ACA GAC TTC GAT GAA GCA TCG AGC GAC TAC GCC GGC CCT GTC CCG CTC Thr Asp Phe Asp Glu Ala Ser Ser Asp Tyr Ala Gly Pro Val Pro Leu 110 115 120	4062
GCG CAA ACT AGA TTG AAG CAT TCG GAT GAA TTT CTT CAG CAC TTC CGA Ala Gln Thr Arg Leu Lys His Ser Asp Glu Phe Leu Gln His Phe Arg 125 130 135	4110
GTT TTA GAC GAT TTG GTG GAG GGG GCT TAC GGG TTT ATC TGC GAC GTC Val Leu Asp Asp Leu Val Glu Gly Ala Tyr Gly Phe Ile Cys Asp Val 140 145 150 155	4158
CGT CGC TAC ACC GAG GAA GAG CAA CGT CGA AGA GGG GTT AAC AGT ACT Arg Arg Tyr Thr Glu Glu Glu Gln Arg Arg Arg Gly Val Asn Ser Thr 160 165 170	4206
AAC CAG GGS AAA TCA AAA TGT AAG CGC CTG ATA GCT AAA TAT GTG AAA Asn Gln Gly Lys Ser Lys Cys Lys Arg Leu Ile Ala Lys Tyr Val Lys 175 180 185	4254
AAT GGA ACA AGG GCG GCC TCT CAG CTG GAA AAT GAA ATT TTG GTT CTC Asn Gly Thr Arg Ala Ala Ser Gln Leu Glu Asn Glu Ile Leu Val Leu 190 195 200	4302
GGG CGC CTA AAT CAC GAG AAT GTT CTC AAG ATC CAG GAA ATC CTT CGG Gly Arg Leu Asn His Glu Asn Val Leu Lys Ile Gln Glu Ile Leu Arg 205 210 215	4350
TAC CCG GAT AAT ACG TAC ATG TTA ACG CAG AGG TAT CAG TTC GAC TTG Tyr Pro Asp Asn Thr Thr Met Leu Thr Gln Arg Tyr Gln Phe Asp Leu 220 225 230 235	4398
TAC AGC TAC ATG TAC GAT GAA GCG TTC GAC TGG AAA GAC AGT CCA ATG Tyr Ser Tyr Met Tyr Asp Glu Ala Phe Asp Trp Lys Asp Ser Pro Met 240 245 250	4446
CTT AAA CAG ACT AGA CGC ATC ATG AAG CAG CTC ATG TCA GCG GTC TCG Leu Lys Gln Thr Arg Arg Ile Met Lys Gln Leu Met Ser Ala Val Ser 255 260 265	4494
TAT ATC CAT TCA AAG AAA CTG ATT CAC AGG GAC ATC AAA CTC GAA AAT Tyr Ile His Ser Lys Lys Leu Ile His Arg Asp Ile Lys Leu Glu Asn 270 275 280	4542
ATT TTC TTA AAC TGC GAC GGC AAG ACA GTG CTG GGC GAC TTT GGA ACT Ile Phe Leu Asn Cys Asp Gly Lys Thr Val Leu Glu Asp Phe Gly Thr 285 290 295	4590

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GTC ACG CCT TTT GAA AAT GAG CGG GAG CCC TTC GAA TAT GGA TGG GTG 4638
Val Thr Pro Phe Glu Asn Glu Arg Glu Pro Phe Glu Tyr Gly Trp Val
300 305 310 315

GGG ACC GTG GCT ACT AAC TCT CCC GAG ATA CTC GCC AGG GAT TCG TAC 4686
Gly Thr Val Ala Thr Asn Ser Pro Glu Ile Leu Ala Arg Asp Ser Tyr
320 325 330

TGT GAA ATT ACA GAC ATT TGG AGC TGC GGA GTA GTA TTG CTG GAA ATG 4734
Cys Glu Ile Thr Asp Ile Trp Ser Cys Gly Val Val Leu Leu Glu Met
335 340 345

GTA AGC CAT GAA TTT TGC CCG ATC GGC GAT GGC GGG GGA AAT CCG CAC 4782
Val Ser His Glu Phe Cys Pro Ile Gly Asp Gly Gly Asn Pro His
350 355 360

CAG CAA TTG CTG AAA GTT ATC GAC TCT CTC TCA GTT TGT GAT GAA GAG 4830
Gln Gln Leu Leu Lys Val Ile Asp Ser Leu Ser Val Cys Asp Glu Glu
365 370 375

TTC CCA GAC CCC CCG TGT AAT CTG TAC AAT TAT TTG CAT TAT GCG AGC 4878
Phe Pro Asp Pro Pro Cys Asn Leu Tyr Asn Tyr Leu His Tyr Ala Ser
380 385 390 395

ATC GAT CGC GCC GGA CAT ACG GTC CCG TCG CTC ATA CGG AAC CTC CAC 4926
Ile Asp Arg Ala Gly His Thr Val Pro Ser Leu Ile Arg Asn Leu His
400 405 410

CTT CCG GCG GAT GTG GAA TAC CCT CTA GTT AAA ATG CTT ACT TTT GAC 4974
Leu Pro Ala Asp Val Glu Tyr Pro Leu Val Lys Met Leu Thr Phe Asp
415 420 425

TGG CGT TTG AGA CCC AGC GCG GCC GAA GTA TTG GCA ATG CCA CTG TTT 5022
Trp Arg Leu Arg Pro Ser Ala Ala Glu Val Leu Ala Met Pro Leu Phe
430 435 440

TCG GCT GAA GAG GAA CGG ACC ATA ACA ATT ATT CAT GGA AAA CAT AAA 5070
Ser Ala Glu Glu Glu Arg Thr Ile Thr Ile Ile His Gly Lys His Lys
445 450 455

CCC ATC CGA CCC GAA ATC CGT GCG CGG GTG CCA CGG TCC ATG AGT GAA 5118
Pro Ile Arg Pro Glu Ile Arg Ala Arg Val Pro Arg Ser Met Ser Glu
460 465 470 475

GGT TAA TAATAAAGGA CGGAGATAGA GAACTGAAGC GTCAGATTTT TTTAAAAAAA 5174
Gly

TAAATGATCG AGAACTTATG ATTTGTCITT CTGTA ATG ACC TTG CCC CAT CGA 5227
Met Thr Leu Pro His Arg
1 5

TTA ACG AAA AGA CCT TTC GCG CGT CGA TTC TGC TCG GTC TTT GTG ATA 5275
Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe Cys Ser Val Phe Val Ile
10 15 20

CAT TAT AGT GAG ACT AAA CTC GAC CGA TAT AAC AAG ACA ATG TTA CTC 5323
His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr Asn Lys Thr Met Leu Leu
25 30 35

TAT AGA CCG GAC TCA ACC ATG CCG CAT AGC GGA GGC GAC GCA AAT CAC 5371
Tyr Arg Pro Asp Ser Thr Met Arg His Ser Gly Gly Asp Ala Asn His
40 45 50

AGA GGG ATA AGG CCG AGG CGG AAA TCT ATT GGA GCG TTT AGC GCG CGC 5419
Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile Gly Ala Phe Ser Ala Arg
55 60 65 70

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GAA AAG ACT GGA AAA CGA AAT GCG CTG ACG GAA AGC AGC TCC TCC TCC Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr Glu Ser Ser Ser Ser Ser	75 80 85	5467
GAC ATG CTA GAT CCG TTT TCC ACG GAT AAG GAA TTT GGC GGT AAG TGG Asp Met Leu Asp Pro Phe Ser Thr Asp Lys Glu Phe Gly Gly Lys Trp	90 95 100	5515
ACG GTA GAC GGA CCT GCC GAC ATT ACT GCC GAG GTC CTT TCT CAG GCA Thr Val Asp Gly Pro Ala Asp Ile Thr Ala Glu Val Leu Ser Gln Ala	105 110 115	5563
TGG GAC GTT CTC CAA TTA GTG AAG CAT GAA GAT GCG GAG GAG GAG AGA Trp Asp Val Leu Gln Leu Val Lys His Glu Asp Ala Glu Glu Glu Arg	120 125 130	5611
GTG ACT TAT GAG TCC AAA CCG ACC CCG ATA CAG CCG TTC AAT GCC TGG Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile Gln Pro Phe Asn Ala Trp	135 140 145 150	5659
CCG GAC GGG CCG AGT TGG AAC GCG CAG GAT TTT ACT CGA GCG CCA ATA Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp Phe Thr Arg Ala Pro Ile	155 160 165	5707
GTT TAT CCC TCT GCG GAG GTA TTG GAC GCA GAG GCG TTG AAA GTA GGG Val Tyr Pro Ser Ala Glu Val Leu Asp Ala Glu Ala Leu Lys Val Gly	170 175 180	5755
GCA TTC GTT AGC CGA GTT TTA CAA TGT GTA CCG TTC ACG CGA TCA AAG Ala Phe Val Ser Arg Val Leu Gln Cys Val Pro Phe Thr Arg Ser Lys	185 190 195	5803
AAA AGC GTT ACG GTG CCG GAT GCG CAG TCG TTT TTG GGG GAC TCG TTC Lys Ser Val Thr Val Arg Asp Ala Gln Ser Phe Leu Gly Asp Ser Phe	200 205 210	5851
TGG AGA ATA ATG CAG AAC GTT TAC ACG GTT GTC TTA CGA CAG CAC ATA Trp Arg Ile Met Gln Asn Val Tyr Thr Val Val Leu Arg Gln His Ile	215 220 225 230	5899
ACT CGA CTC AGG CAC CCT TCC AGC AAA AGC ATT GTT AAC TGC AAC GAC Thr Arg Leu Arg His Pro Ser Ser Lys Ser Ile Val Asn Cys Asn Asp	235 240 245	5947
CCT CTA TGG TAC GCC TAC GCG AAT CAA TTT CAC TGG AGA GGA ATG CGC Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe His Trp Arg Gly Met Arg	250 255 260	5995
GTG CCG TCG CTT AAA TTA GCC TCT CCC CCG GAG GAG AAT ATT CAA CAC Val Pro Ser Leu Lys Leu Ala Ser Pro Pro Glu Glu Asn Ile Gln His	265 270 275	6043
GGC CCA ATG GCC GCC GTT TTT AGA AAC GCG GGG GCT GGT CTG TTC CTG Gly Pro Met Ala Ala Val Phe Arg Asn Ala Gly Ala Gly Leu Phe Leu	280 285 290	6091
TGG CCT GCC ATG CGC GCA GCC TTT GAA GAG CGC GAC AAG CGA CTG TTA Trp Pro Ala Met Arg Ala Ala Phe Glu Glu Arg Asp Lys Arg Leu Leu	295 300 305 310	6139
AGA GCA TGC CTG TCT TCA CTC GAT ATC ATG GAC GCA GCC GTC CTC GCG Arg Ala Cys Leu Ser Ser Leu Asp Ile Met Asp Ala Ala Val Leu Ala	315 320 325	6187
TCG TTT CCA TTT TAC TGG CGC GGC GTC CAA GAC ACC TCG CGC TTC GAG Ser Phe Pro Phe Tyr Trp Arg Gly Val Gln Asp Thr Ser Arg Phe Glu	330 335 340	6235

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CCT GCG CTG GGC TGT TTG TCA GAG TAC TTT GCA CTA GTG GTG TTA CTG Pro Ala Leu Gly Cys Leu Ser Glu Tyr Phe Ala Leu Val Val Leu Leu 345 350 355	6283
GCC GAG ACG GTC TTA GCG ACC ATG TTC GAC CAC GCA CTG GTA TTC ATG Ala Glu Thr Val Leu Ala Thr Met Phe Asp His Ala Leu Val Phe Met 360 365 370	6331
AGG GCG CTG GCA GAC GGC AAT TTC GAT GAC TAT GAC GAA ACT AGA TAT Arg Ala Leu Ala Asp Gly Asn Phe Asp Asp Tyr Asp Glu Thr Arg Tyr 375 380 385	6379
ATA GAC CCC GTT AAA AAC GAG TAC CTG AAC GGA GCC GAG GGT ACT CTG Ile Asp Pro Val Lys Asn Glu Tyr Leu Asn Gly Ala Glu Gly Thr Leu 395 400 405	6427
TTA CGG GGC ATA GTG GCC TCC AAC ACC GCT CTG GCG GTG GTT TGC GCA Leu Arg Gly Ile Val Ala Ser Asn Thr Ala Leu Ala Val Val Cys Ala 410 415 420	6475
AAC ACC TAT TCG ACG ATA AGA AAA CTC CCG TCC GTG GCA ACT AGC GCG Asn Thr Tyr Ser Thr Ile Arg Lys Leu Pro Ser Val Ala Thr Ser Ala 425 430 435	6523
TGC AAT GTT GCC TAC AGG ACC GAA ACG CTG AAA GCG AGG CGC CCT GGC Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu Lys Ala Arg Arg Pro Gly 440 445 450	6571
ATG AGC GAC ATA TAC CGG ATA TTA CAA AAA GAG TTT TTC TTT TAC ATT Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys Glu Phe Phe Thr Tyr Ile 455 460 465 470	6619
GCG TGG CTC CAG AGG GTT GCA ACA CAC GCA AAT TTC TGT TTA AAC ATT Ala Trp Leu Gln Arg Val Ala Thr His Ala Asn Phe Cys Leu Asn Ile 475 480 485	6667
CTG AAG AGA AGC GTG GAT ACG GGG GCC CCG CCA TTT TTG TTC AGG GCC Leu Lys Arg Ser Val Asp Thr Gly Ala Pro Pro Phe Leu Phe Arg Ala 490 495 500	6715
AGC TCG GAG AAG CGG CTG CAG CAG TTA AAT AAA ATG CTC TGC CCC CTT Ser Ser Glu Lys Arg Leu Gln Gln Leu Asn Lys Met Leu Cys Pro Leu 505 510 515	6763
CTC GTG CCG ATT CAA TAT GAA GAC TTT TCG AAG GCC ATG GGG TCT GAG Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser Lys Ala Met Gly Ser Glu 520 525 530	6811
CTC AAG AGG GAA AAG TTA GAG ACA TTC GTT AAA GCT ATT TCC AGC GAC Leu Lys Arg Glu Lys Leu Glu Thr Phe Val Lys Ala Ile Ser Ser Asp 535 540 545 550	6859
AGG GAC CCG AGG GGG TCC TTA AGA TTT CTC ATT TCG GAC CAT GCA AGG Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu Ile Ser Asp His Ala Arg 555 560 565	6907
GAA ATT ATT GCA GAC GGA GTA CGG TTT AAG CCG GTG ATA GAC GAG CCG Glu Ile Ile Ala Asp Gly Val Arg Phe Lys Pro Val Ile Asp Glu Pro 570 575 580	6955
GTT CGG GCT TCA GTT GCG CTG AGT ACC GCT GCC GCT GGG AAA GTG AAA Val Arg Ala Ser Val Ala Leu Ser Thr Ala Ala Ala Gly Lys Val Lys 585 590 595	7003
GCG CGA CGC TTA ACC TCA GTT CGC GCG CCC GTA CCG GGC GCA GGC GCC Ala Arg Arg Leu Thr Ser Val Arg Ala Pro Val Pro Gly Ala Gly Ala 600 605 610	7051

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GTT TCC GCG CGC CGG AAA TCG GAA ATA TGA TAAAAATGCT TGGCATTTCG 7101
 Val Ser Ala Arg Arg Lys Ser Glu Ile
 615 620
 GGGCGAAGAG GCGTGATCTG AAGGGCTCCA CAATGACGTA ACTGAGCTAC GCATCCCTAT 7161
 AAAGTGATACC CGCTGACGCG TAGCCATAC AGTGTTACAG GAGGGGAGAG AGACAAC TTC 7221
 AGCTCGAAGT CTGAAGAGAC ATC ATG AGC GGC TTC AGT AAC ATA GGA TCG 7271
 Met Ser Gly Phe Ser Asn Ile Gly Ser
 1 5
 ATT GCC ACC GTT TCC CTA GTA TGC TCG CTT TTG TGC GCA TCT GTA TTA 7319
 Ile Ala Thr Val Ser Leu Val Cys Ser Leu Leu Cys Ala Ser Val Leu
 10 15 20 25
 GGG GCG CCG GTA CTG GAC GGG CTC GAG TCG AGC CCT TTC CCG TTC GGG 7367
 Gly Ala Pro Val Leu Asp Gly Leu Glu Ser Ser Pro Phe Pro Phe Gly
 30 35 40
 GGC AAA ATT ATA GCC CAG GCG TGC AAC CGC ACC ACG ATT GAG GTG ACG 7415
 Gly Lys Ile Ile Ala Gln Ala Cys Asn Arg Thr Thr Ile Glu Val Thr
 45 50 55
 GTC CCG TGG AGC GAC TAC TCT GGT CGC ACC GAA GGA GTG TCA GTC GAG 7463
 Val Pro Trp Ser Asp Tyr Ser Gly Arg Thr Glu Gly Val Ser Val Glu
 60 65 70
 GTG AAA TGG TTC TAC GGG AAT AGT AAT CCC GAA AGC TTC GTG TTC GGG 7511
 Val Lys Trp Phe Tyr Gly Asn Ser Asn Pro Glu Ser Phe Val Phe Gly
 75 80 85
 GTG GAT AGC GAA ACG GGC AGT GGA CAC GAG GAC CTG TCT ACG TGC TGG 7559
 Val Asp Ser Glu Thr Gly Ser Gly His Glu Asp Glu Ser Thr Cys Trp
 90 95 100 105
 GCT CTA ATC CAT AAT CTG AAC GCG TCT GTG TGC AGG GCG TCT GAC GCC 7607
 Ala Leu Ile His Asn Leu Asn Ala Ser Val Cys Arg Ala Ser Asp Ala
 110 115 120
 GGG ATA CCT GAT TTC GAC AAG CAG TGC GAA AAA GTG CAG AGA AGA CTG 7655
 Gly Ile Pro Asp Phe Asp Lys Gln Cys Glu Lys Val Gln Arg Arg Leu
 125 130 135
 CGC TCC GGG GTG GAA CTT GGT AGT TAC GTG TCT GGC AAT GGA TCC CTG 7703
 Arg Ser Gly Val Glu Leu Gly Ser Tyr Val Ser Gly Asn Gly Ser Leu
 140 145 150
 GTG CTG TAC CCA GGG ATG TAC GAT GCC GGC ATC TAC GCC TAC CAG CTC 7751
 Val Leu Tyr Pro Gly Met Tyr Asp Ala Gly Ile Tyr Ala Tyr Gln Leu
 155 160 165
 TCA GTG GGT GGG AAG GGA TAT ACC GGG TCT GTT TAT CTA GAC GTC GGA 7799
 Ser Val Gly Gly Lys Gly Tyr Thr Gly Ser Val Tyr Leu Asp Val Gly
 170 175 180 185
 CCA AAC CCC GGA TGC CAC GAC CAG TAT GGG TAC ACC TAT TAC AGC CTG 7847
 Pro Asn Pro Gly Cys His Asp Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu
 190 195 200
 GCC GAC GAG GCG TCA GAC TTA TCA TCT TAT GAC GTA GCC TCG CCC GAA 7895
 Ala Asp Glu Ala Ser Asp Leu Ser Ser Tyr Asp Val Ala Ser Pro Glu
 205 210 215
 CTC GAC GGT CCT ATG GAG GAA GAT TAT TCC AAT TGT CTA GAC ATG CCC 7943
 Leu Asp Gly Pro Met Glu Glu Asp Tyr Ser Asn Cys Leu Asp Met Pro
 220 225 230

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CCG CTA CGC CCA TGG ACA ACC GTT TGT TCG CAT GAC GTC GAG GAG CAG Pro Leu Arg Pro Trp Thr Thr Val Cys Ser His Asp Val Glu Glu Gln 235 240 245	7991
GAA AAC GCC ACG GAC GAG CTT TAC CTA TGG GAC GAG GAA TGC GCC GGT Glu Asn Ala Thr Asp Glu Leu Tyr Leu Trp Asp Glu Glu Cys Ala Gly 250 255 260 265	8039
CCG CTG GAC GAG TAC GTC GAC GAA AGG TCA GAG ACG ATG CCC AGG ATG Pro Leu Asp Glu Tyr Val Asp Glu Arg Ser Glu Thr Met Pro Arg Met 270 275 280	8087
GTT GTC TTT TCA CCG CCC TCT ACG CTC CAG CAG TAG CCACCCGAGA Val Val Phe Ser Pro Pro Ser Thr Leu Gln Gln 285 290	8133
GTGTTTTTTG TGAGCGCCCA CGCAACATAC CTAACCTGCTT CATTTCTGAT CAATTATTGC	8193
GTATTGAATA AATAAACAGT ACAAAAGCAT CAGGTGTGGT TTGCGTGTCT GTGCTAAACC	8253
ATGGCGTGTG CGGTGAAAC CGTAAATTAC GTGATAATAA ATAGCATAGG AGTTGGCGTG	8313
CAGCGTATTT CGCCGAGAGA TGGGGACAAT GTTAGTGTG CGCCTTTTCC TACTTGCAGT	8373
AGCGGACGCG GCGTTGCCGA CCGGCAGATT CTGCCGAGTT TGAAGGTGC CTCGGGAGG	8433
AACCATCAA GAGAACCTGG CCGTGCTCGC GGAATCGCCG GTCACGGAC ACGCGACATA	8493
TCCGCCGCCT GAAGGCGCCG TCAGCTTTCA GATTTTTGCG GACACCCCTA CTTTGGCGAT	8553
TCGCTACGGC GCTACGGAGG ACGAACTTGC ACTGGAGCGC GGGACGTCCG CCTCAGACGC	8613
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CACCATAGGG GTATTTCGCTA CTGGCCAGAG CACGGAAGC AGCTATTCCG TCATCAGTCG	8733
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TGTGCGAGAT AACGATGTCT CCGTGTGAC AAAAGCGCAG TACATTGGGG AGTGCTACTC	8913
CAACTCGGCG GCCCAGACGG GGCTCACGTC TCTCAACATG ACCTTTTTCT ATTGCGCTAA	8973
AAGAATAGTA AACGTCACGT GGACAACCG CGGCCCTCC CCCTCGCGCA TAACGGTATA	9033
CTCGTCGCGG GAGAACGGGC AGCCCGTGT GAGGAACGTT TCTGACGGT TCTTGGTTAA	9093
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GGACTCCGCG AGCGTCCTCG CGTTTACGGC CTTTAGGGAA GGAAGACTCC ATCCGCGAT	9213
TCAACTGCAC CGGATAGATA TGTCCGGGAC TGAGCCGCGG GGGACTGAAA CGACCTTCCA	9273
CTGTCAAAAA ATGATAGAAA CCCCCTACCG AGCGCTCGGG AGCAATGTTT CCAGGGACGA	9333
CTCTATCCGT CCGGGGGCCA CTCTGCCTCC GTTCGATACC GCAGCACCTG ATTTCGATAC	9393
AGGTACTTCC CCGACCCCCA CTACCGTGCC AGAGCCAGCC ATTACTACAC TCATACCGCG	9453
CAGCACTAGC GATATGGGAT TCTTCTCCAC GGCACGTGCT ACCGGATCAG AAACCTTTTC	9513
GGTACCCTGC CAGGAAACGG ATAGAATCTT TTCGACAACT CCTCTTACCC TTCCACTGAC	9573
TCCCGGTGAG TCAGAAAATA CACTGTTTCC TACGACCGCG CCGGGGATTT CTACCGAGAC	9633
CCCGAGCGCG GCACATGAAA CTACACAGAC CCAGAGTGCA GAAACGGTGG TCTTTACTCA	9693

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GAGTCCGAGT ACCGAGTCGG AAACCGCGCG GTCCAGAGT CAGGAACCGT GGTATTTTAC 9753
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 GGAAATTACT CAGACCCGGA GCGCGGCACC GGAGGTTTAT ACTCGGAGTT CGAGTACGAT 10353
 GCCAGAACT GCACAGAGCA CACCCCTGGC CTCGAAAAA CCTACCAAGT CGGGAACCGG 10413
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 AACATCGGTC CAGCTAATGT GCCTGTCGTG CAGGAGCCAT TCTCCGGAAC CTACTGTCT 10833
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 TACAGGGAAT GTGGCAGCT ACAACTGCTA TCTGAATGCG CCGTTCAATC TGCACAGATG 11670
 TGGCGAGTGG ACTATGTTC TAGCACCTT GTATCGCGAA ATGGCGCGGG ACTGACTATA 11730

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TCTCTCCCCA CTGCTGCGCT CTCTGGCCAA TACTTGCTGA CCCTGAAAT CGGGAGATT	11790
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CTTAACCTTTT TACCGTCGAA ATGCTGGACA ACAGAACAGT ATCAGACTGG ATTTCAAGGC	11910
GAACACCTTT ATCCGATCGC AGACACCAAT ACACGACACG CGGACGACGT ATATCGGGGA	11970
TACGAAGATA TTCTGCAGCG CTGGAATAAT TTGCTGAGGA AAAAGAATCC TAGCGCGCCA	12030
GACCCCTGTC CAGATAGCGT CCCGCAAGAA ATTCCCGCTG TAACCAAGAA AGCGGAAGGG	12090
CGCACCCCGG ACGCAGAAAG CAGCGAAAAG AAGGCCCTC CAGAAGACTC GGAGGACGAC	12150
ATGCAGGCAG AGGCTTCTGG AGAAAATCCT GCCGCCCTCC CCGAAGACGA CGAAGTCCCC	12210
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GCGTTCGTAG CCTGCGCGGT CGCGCTCGTG GGGCTACTGG TTTGGAGCAT CGTAAAATGC	12390
GCGCGTAGCT AA TCGAGCCTAG AATAGGTGGT TTCTTCCTAC ATGCCACGCC	12442
TCACGCTCAT AATATAAATC ACATGGAATA GCATACCAAT GCCTATTTCAT TGGGACGTTT	12502
GAAAAGC ATG GCA TCG CTA CTT GGA ACT CTG GCT CTC CTT GCC GCG ACG Met Ala Ser Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr	12551
CTC GCA CCC TTC GGC GCG ATG GGA ATC GTG ATC ACT GGA AAT CAC GTC Leu Ala Pro Phe Gly Ala Met Gly Ile Val Ile Thr Gly Asn His Val	12599
TCC GCC AGG ATT GAC GAC GAT CAC ATC GTG ATC GTC GCG CCT CGC CCC Ser Ala Arg Ile Asp Asp Asp His Ile Val Ile Val Ala Pro Arg Pro	12647
GAA GCT ACA ATT CAA CTG CAG CTA TTT TTC ACT CCT GGC CAG AGA CCC Glu Ala Thr Ile Gln Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro	12695
CAC AAA CCC TAC TCA GGA ACC GTC CGC GTC GCG TTT CGG TCT GAT ATA His Lys Pro Tyr Ser Gly Thr Val Arg Val Ala Phe Arg Ser Asp Ile	12743
ACA AAC CAG TGC TAC CAG GAA CTT AGC GAG GAG CGC TTT GAA AAT TGC Thr Asn Gln Cys Tyr Gln Glu Leu Ser Glu Glu Arg Phe Glu Asn Cys	12791
ACT CAT CGA TCG TCT TCT GTT TTT GTC GGC TGT AAA GTG ACC GAG TAC Thr His Arg Ser Ser Ser Val Phe Val Gly Cys Lys Val Thr Glu Tyr	12839
ACG TTC TCC GCC TCG AAC AGA CTA ACC GGA CCT CCA CAC CCG TTT AAG Thr Phe Ser Ala Ser Asn Arg Leu Thr Gly Pro Pro His Pro Phe Lys	12887
CTC ACT ATA CGA AAT CCT CGT CCG AAC GAC AGC GGG ATG TTC TAC GTA Leu Thr Ile Arg Asn Pro Arg Pro Asn Asp Ser Gly Met Phe Tyr Val	12935
ATT GTT CGG CTA GAC GAC ACC AAA GAA CCC ATT GAC GTC TTC GCG ATC Ile Val Arg Leu Asp Asp Thr Lys Glu Pro Ile Asp Val Phe Ala Ile	12983

CAA CTA TCG GTG TAT CAA TTC GCG AAC ACC GCC GCG ACT CGC GGA CTC Gln Leu Ser Val Tyr Gln Phe Ala Asn Thr Ala Thr Arg Gly Leu 160 165 170	13031
TAT TCC AAG GCT TCG TGT CGC ACC TTC GGA TTA CCT ACC GTC CAA CTT Tyr Ser Lys Ala Ser Cys Arg Thr Phe Gly Leu Pro Thr Val Gln Leu 175 180 185 190	13079
GAG GCC TAT CTC AGG ACC GAG GAA AGT TGG CGC AAC TGG CAA GCG TAC Glu Ala Tyr Leu Arg Thr Glu Glu Ser Trp Arg Asn Trp Gln Ala Tyr 195 200 205	13127
GTT GCC ACG GAG GCC ACG ACG ACC AGC GCC GAG GCG ACA ACC CCG ACG Val Ala Thr Glu Ala Thr Thr Thr Ser Ala Glu Ala Thr Pro Thr 210 215 220	13175
CCC GTC ACT GCA ACC AGC GCC TCC GAA CTT GAA GCG GAA CAC TTT ACC Pro Val Thr Ala Thr Ser Ala Ser Glu Leu Glu Ala Glu His Phe Thr 225 230 235	13223
TTT CCC TGG CTA GAA AAT GGC GTG GAT CAT TAC GAA CCG ACA CCC GCA Phe Pro Trp Leu Glu Asn Gly Val Asp His Tyr Glu Pro Thr Pro Ala 240 245 250	13271
AAC GAA AAT TCA AAC GTT ACT GTC CST CTC GGG ACA ATG AGC CCT ACG Asn Glu Asn Ser Asn Val Thr Val Arg Leu Gly Thr Met Ser Pro Thr 255 260 265 270	13319
CTA ATT GGG GTA ACC GTG GCT GCC GTC GTG AGC GCA ACG ATC GGC CTC Leu Ile Gly Val Thr Val Ala Ala Val Val Ser Ala Thr Ile Gly Leu 275 280 285	13367
GTC ATT GTA ATT TCC ATC GTC ACC AGA AAC ATG TGC ACC CCG CAC CGA Val Ile Val Ile Ser Ile Val Thr Arg Asn Met Cys Thr Pro His Arg 290 295 300	13415
AAA TTA GAC ACG GTC TCG CAA GAC GAC GAA GAA CGT TCC CAA ACT AGA Lys Leu Asp Thr Val Ser Gln Asp Asp Glu Glu Arg Ser Gln Thr Arg 305 310 315	13463
AGG GAA TCG CGA AAA TTT GGA CCC ATG GTT GCG TGC GAA ATA AAC AAG Arg Glu Ser Arg Lys Phe Gly Pro Met Val Ala Cys Glu Ile Asn Lys 320 325 330	13511
GGG GCT GAC GAC GAT AGT GAA CTT GTG GAA CTG GTT GCG ATT GTT AAC Gly Ala Asp Gln Asp Ser Glu Leu Val Glu Leu Val Ala Ile Val Asn 335 340 345 350	13559
CCG TCT GCG CTA AGC TCG CCC GAC TCA ATA AAA ATG TGA TTAAGTCTGA Pro Ser Ala Leu Ser Ser Pro Asp Ser Ile Lys Met 355 360	13608
ATGTGGCTCT CCAATCATTT CGATTCTCTA ATCTCCCAAT CCTCTCAAAA GGGGCAGTAT	13668
CGGACACGGA CTGGGAGGGG CGTACACGAT AGTTATATGG TACAGCAGAG GCCTCTGAAC	13728
ACTTAGGAGG AGAATTGAGC CGGGGAGAGC CCCTGTTGAG TAGGCTTGGG AGCATATTGC	13788
AGG ATG AAC ATG TTA GTG ATA GTT CTC GCC TCT TGT CTT GCG CGC CTA Met Asn Met Leu Val Ile Val Leu Ala Ser Cys Leu Ala Arg Leu 1 5 10 15	13836
ACT TTT GCG ACG CGA CAC GTC CTC TTT TTG GAA GGC ACT CAG GCT GTC Thr Phe Ala Thr Arg His Val Leu Phe Leu Glu Gly Thr Gln Ala Val 20 25 30	13884

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CTC GGG GAA GAT GAT CCC AGA AAC GTT CCG GAA GGG ACT GTA ATC AAA Leu Gly Glu Asp Asp Pro Arg Asn Val Pro Glu Gly Thr Val Ile Lys 35 40 45	13932
TGG ACA AAA GTC CTG CGG AAC GCG TGC AAG ATG AAG GCG GCC GAT GTC Trp Thr Lys Val Leu Arg Asn Ala Cys Lys Met Lys Ala Ala Asp Val 50 55 60	13980
TGC TCT TCG CCT AAC TAT TGC TTT CAT GAT TTA ATT TAC GAC GGA GGA Cys Ser Ser Pro Asn Tyr Cys Phe His Asp Leu Ile Tyr Asp Gly Gly 65 70 75	14028
AAG AAA GAC TGC CCG CCC GCG GGA CCC CTG TCT GCA AAC CTG GTA ATT Lys Lys Asp Cys Pro Ala Gly Pro Leu Ser Ala Asn Leu Val Ile 80 85 90 95	14076
TTA CTA AAG GCG GGC GAA AGC TTC GTC GTG CTG GGT TCT GGS CTA CAC Leu Leu Lys Arg Gly Glu Ser Phe Val Val Leu Gly Ser Gly Leu His 100 105 110	14124
AAC AGC AAT ATA ACT AAT ATC ATG TGG ACA GAG TAC GGA GGC CTG CTC Asn Ser Asn Ile Thr Asn Ile Met Trp Thr Glu Tyr Gly Gly Leu Leu 115 120 125	14172
TTT GAT CCT GTA ACT CGT TCG GAC GAG GGA ATC TAT TTT CGA CGG ATC Phe Asp Pro Val Thr Arg Ser Asp Glu Gly Ile Tyr Phe Arg Arg Ile 130 135 140	14220
TCT CAG CCA GAT CTG GCC ATG GAA ACT ACA TCG TAC AAC GTC AGC GTT Ser Gln Pro Asp Leu Ala Met Glu Thr Thr Ser Tyr Asn Val Ser Val 145 150 155	14268
CTT TCG CAC GTA GAC GAG AAG GCT CCA GCA CCG CAC GAG GTG GAG ATA Leu Ser His Val Asp Glu Lys Ala Pro Ala Pro His Glu Val Glu Ile 160 165 170 175	14316
GAC ACC ATT AAG CCG TCA GAG GCC CAC GCG CAC GTG GAA TTA CAA ATG Asp Thr Ile Lys Pro Ser Glu Ala His Ala His Val Glu Leu Gln Met 180 185 190	14364
CTG CCG TTT CAT GAA CTC AAC GAC AAC AGC CCC ACC TAT GTG ACC CCT Leu Pro Phe His Glu Leu Asn Asp Asn Ser Pro Thr Tyr Val Thr Pro 195 200 205	14412
GTT CTT AGA GTC TTC CCA CCG ACC GAG CAC GTA AAA TTT AAC GTT ACG Val Leu Arg Val Phe Pro Pro Thr Glu His Val Lys Phe Asn Val Thr 210 215 220	14460
TAT TCG TGG TAT GGG TTT GAT GTC AAA GAG GAG TGC GAA GAA GTG AAA Tyr Ser Trp Tyr Gly Phe Asp Val Lys Glu Glu Cys Glu Glu Val Lys 225 230 235	14508
CTG TTC GAG CCG TGC GTA TAC CAT CCT ACA GAC GGC AAA TGT CAG TTT Leu Phe Glu Pro Cys Val Tyr His Pro Thr Asp Gly Lys Cys Gln Phe 240 245 250 255	14556
CCC GCA ACC AAC CAG AGA TGC CTC ATA GGA TCT GTC TTG ATG GCG GAA Pro Ala Thr Asn Gln Arg Cys Leu Ile Gly Ser Val Leu Met Ala Glu 260 265 270	14604
TTC TTG GGC GCG GCC TCT TTG CTG GAT TGT TCC CGC GAT ACT CTA GAA Phe Leu Gly Ala Ala Ser Leu Leu Asp Cys Ser Arg Asp Thr Leu Glu 275 280 285	14652
GAC TGC CAC GAA AAT CGC GTG CCG AAC CTA CGG TTC GAT TCG CGA CTC Asp Cys His Glu Asn Arg Val Pro Asn Leu Arg Phe Asp Ser Arg Leu 290 295 300	14700

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TCC GAG TCA CGC GCA GGC CTG GTG ATC AGT CCT CTT ATA GCC ATC CCC Ser Glu Ser Arg Ala Gly Leu Val Ile Ser Pro Leu Ile Ala Ile Pro 305 310 315	14748
AAA GTT TTG ATT ATA GTC GTT TCC GAC GGA GAC ATT TTG GGA TGG AGC Lys Val Leu Ile Ile Val Val Ser Asp Gly Asp Ile Leu Gly Trp Ser 320 325 330 335	14796
TAC ACG GTG CTC GGG AAA CGT AAC AGT CCG CGC GTA GTA GTC GAA ACG Tyr Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Gly Thr 340 345 350	14844
CAC ATG CCC TCG AAG GTC CCG ATG AAC AAA GTA GTA ATT GGC AGT CCC His Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro 355 360 365	14892
GGA CCA ATG GAC GAA ACG GGT AAC TAT AAA ATG TAC TTC GTC GTC GCG Gly Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala 370 375 380	14940
GGG GTG GCC GCG ACG TGC GTA ATT CTT ACA TGC GCT CTG CTT GTG GGG Gly Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly 385 390 395	14988
AAA AAG AAG TGC CCC GCG CAC CAA ATG GGT ACT TTT TCC AAG ACC GAA Lys Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu 400 405 410 415	15036
CCA TTG TAC GCG CCG CTC CCC AAA AAC GAG TTT GAG GCC GGC GGG CTT Pro Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu 420 425 430	15084
ACG GAC GAT GAG GAA GTG ATT TAT GAC GAA GTA TAC GAA CCC CTA TTT Thr Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe 435 440 445	15132
CGC GGC TAC TGT AAG CAG GAA TTC CGC GAA GAT GTG AAT ACC TTT TTC Arg Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe 450 455 460	15180
GGT GCG GTC GTG GAG GGA GAA AGG GCC TTA AAC TTT AAA TCC GCC ATC Gly Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile 465 470 475	15228
GCA TCA ATG GCA GAT CGC ATC CTG GCA AAT AAA AGC GGC AGA AGG AAT Ala Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn 480 485 490 495	15276
ATG GAT AGC TAT TAG TTGTC ATG CCT TTT AAG ACC AGA GGC GCC GAA Met Asp Ser Tyr 500 Met Pro Phe Lys Thr Arg Gly Ala Glu 5	15324
GAC GCG GCC GCG GGC AAG AAC AGG TTT AAG AAA TCG AGA AAT CGG GAA Asp Ala Ala Ala Gly Lys Asn Arg Phe Lys Lys Ser Arg Asn Arg Glu 25 10 15 20	15372
ATC TTA CCG ACC AGA CTG CGT GGC ACC GGT AAG AAA ACT GCC GGA TTG Ile Leu Pro Thr Arg Leu Arg Gly Thr Gly Lys Lys Thr Ala Gly Leu 30 35 40	15420
TCC AAT TAT ACC CAG CCT ATT CCC TGG AAC CCT AAA TTC TGC AGC GCG Ser Asn Tyr Thr Gln Pro Ile Pro Trp Asn Pro Lys Phe Cys Ser Ala 55 45 50	15468
CGC GGG GAA TCT GAC AAC CAC GCG TGT AAA GAC ACT TTT TAT CGC AGG Arg Gly Glu Ser Asp Asn His Ala Cys Lys Asp Thr Phe Tyr Arg Arg 70 60 65 70	15516

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ACG TGC TGC GCA TCG CGC TCT ACC GTT TCC AGT CAA CCC GAT TCC CCC 15564
Thr Cys Cys Ala Ser Arg Ser Thr Val Ser Ser Gln Pro Asp Ser Pro
75 80 85

CAC ACA CCC ATG CCT ACT GAG TAT GGG CGC GTG CCC TCC GCA AAG CGC 15612
His Thr Pro Met Pro Thr Glu Tyr Gly Arg Val Pro Ser Ala Lys Arg
90 95 100 105

AAA AAA CTA TCA TCT TCA GAC TGC GAG GGC GCG CAC CAA CCC CTA GTA 15660
Lys Lys Leu Ser Ser Ser Asp Cys Glu Gly Ala His Gln Pro Leu Val
110 115 120

TCC TGT AAA CTT CCG GAT TCT CAA GCA GCA CCG GCG CGA ACC TAT AGT 15708
Ser Cys Lys Leu Pro Asp Ser Gln Ala Ala Pro Ala Arg Thr Tyr Ser
125 130 135

TCT GCG CAA AGA TAT ACT GTT GAC GAG GTT TCG TCG CCA ACT CCG CCA 15756
Ser Ala Gln Arg Tyr Thr Val Asp Glu Val Ser Ser Pro Thr Pro Pro
140 145 150

GGC GTC GAC GCT GTT GCG GAC TTA GAA ACG CGC GCG GAA CTT CCT GGC 15804
Gly Val Asp Ala Val Ala Asp Leu Glu Thr Arg Ala Glu Leu Pro Gly
155 160 165

GCT ACG ACG GAA CAA ACG GAA AGT AAA AAT AAG CTC CCC AAC CAA CAA 15852
Ala Thr Thr Glu Gln Thr Glu Ser Lys Asn Lys Leu Pro Asn Gln Gln
170 175 180 185

TCG CGC CTG AAG CCG AAA CCC ACA AAC GAG CAC GTC GGA GGG GAG CGG 15900
Ser Arg Leu Lys Pro Lys Pro Thr Asn Glu His Val Gly Glu Arg
190 195 200

TGC CCC TCC GAA GGC ACG GTC GAG GCG CCA TCG CTC GGC ATC CTC TCG 15948
Cys Pro Ser Glu Gly Thr Val Glu Ala Pro Ser Leu Gly Ile Leu Ser
205 210 215

CGC GTC GGG GCA GCG ATA GCA AAC GAG CTG GCT CGT ATG CCG AGG GCG 15996
Arg Val Gly Ala Ala Ile Ala Asn Glu Leu Ala Arg Met Arg Arg Ala
220 225 230

TGT CTT CCG CTC GCC GCG TCG GCG GCC GCT GCC GGA ATA GTG GCC TGG 16044
Cys Leu Pro Leu Ala Ala Ser Ala Ala Ala Gly Ile Val Ala Trp
235 240 245

GCC GCG GCG AGG GCC TTG CAG AAA CAA GGG CGG TAG CAGTAATAAT 16090
Ala Ala Ala Arg Ala Leu Gln Lys Gln Gly Arg
250 255 260

AACCACACAA ATATTGACAA TAATAAACGC GTACGCGG ATG AGT AAG TGT TAT 16143
Met Ser Lys Cys Tyr
1 5

TGT CTC GCG CGC CAT CTT TAT AAA AGC CCG CGT TGC GTG GGC CGG CGG 16191
Cys Leu Ala Arg His Leu Tyr Lys Ser Pro Arg Cys Val Gly Arg
10 15 20

GTA GCA TTT GGA GGG TTG GCG ACC ATG TCG AGA CCT CCG ACG TCA CAT 16239
Val Ala Phe Gly Gly Leu Ala Thr Met Ser Arg Pro Pro Thr Ser His
25 30 35

TTG GAC TTA GCT TTC TCG GCG GCC TTT AGG GGC ACG GAC CTG CCC GGA 16287
Leu Asp Leu Ala Phe Ser Ala Ala Phe Arg Gly Thr Asp Leu Pro Gly
40 45 50

GGG AGA TTC TGG CGG GCG TCG CAG AGT TGC GAT ATT TTC TTT TGG CCC 16335
Gly Arg Phe Trp Arg Ala Ser Gln Ser Cys Asp Ile Phe Phe Trp Pro
55 60 65

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GAT CTG GCC GCG GTG ATC GTA CAG GCC GCC CGC GCG TAT TTT GAA GGG Asp Leu Ala Ala Val Ile Val Gln Ala Ala Arg Ala Tyr Phe Glu Gly 70 75 80 85	16383
AAG GAA AGG CTG GGC AGT CTG CAG GTC GCC GAA GAT ATC ACG GCG CAC Lys Glu Arg Leu Gly Ser Leu Gln Val Ala Glu Asp Ile Thr Ala His 90 95 100	16431
GAC CCG CGA ATA GCG CCC GCG GCT AAG CGC GCC GTC GCA GCG GCG GTA Asp Pro Arg Ile Ala Pro Ala Ala Lys Arg Ala Val Ala Ala Val 105 110 115	16479
GGA CTG TGG ACC GCG CTG TCG GAG TTA GTT GGG GGG CCG AAC GGG GAG Gly Leu Trp Thr Ala Leu Ser Glu Leu Val Gly Gly Pro Asn Gly Glu 120 125 130	16527
TTG GAA AGC AAG GTC TGG GGC AAG CAG ATT CCC CGG GCC GCC GCG TGG Leu Glu Ser Lys Val Trp Gly Lys Gln Ile Pro Arg Ala Ala Trp 135 140 145	16575
GAA ATA AGA GAC GTG CCC AAA GTT CCA GTC ATT GGG CCG GAC ATT CTT Glu Ile Arg Asp Val Pro Lys Val Pro Val Ile Gly Pro Asp Ile Leu 150 155 160 165	16623
TCT TTT TTC TCC GCC GCC GTC GAG CTG CCG GTG CTC TAT ATC AGA GCC Ser Phe Phe Ser Ala Ala Val Glu Leu Pro Val Leu Tyr Ile Arg Ala 170 175 180	16671
CGG GGA GGG GCG CAC TCG CGG TCC GCG CAC TGG AAT AAC CAG AGC AGC Arg Gly Gly Ala His Ser Arg Ser Ala His Trp Asn Asn Gln Ser Ser 185 190 195	16719
GCG CCG GCC GCC GGA CTC GCG GCG ATA AGG ATA GGC ATG GAG ATG GTG Ala Pro Ala Ala Gly Leu Ala Ala Ile Arg Ile Gly Met Glu Met Val 200 205 210	16767
CGG AGC CTC CTG GTG ATA GCG CTG CCT CTG TCA AAC TTC ACC CTC CCG Arg Ser Leu Leu Val Ile Ala Leu Pro Leu Ser Asn Phe Thr Leu Pro 215 220 225	16815
GAA GAC CTC CCC GAA GGT TCC CAA AAC TCG ATC CGC GCG TTC GTG GCC Glu Asp Leu Pro Glu Gly Ser Gln Asn Ser Ile Arg Ala Phe Val Ala 230 235 240 245	16863
CAC CTC ATG AAC TGT GTA GCT ACC GAT AAG ATC ATG TCT CCG GAC GTG His Leu Met Asn Cys Val Ala Thr Asp Lys Ile Met Ser Pro Asp Val 250 255 260	16911
CGC GTC CCA GTC GAA GAA AGC TTT TAC AGC CAC TGT TTA AGG GAA ATC Arg Val Pro Val Glu Glu Ser Phe Tyr Ser His Cys Leu Arg Glu Ile 265 270 275	16959
ATT ATG TGC GAG AGA GCT TTT TGT TAC CCG TGC AAT CCC CCG CCA AAA Ile Met Cys Glu Arg Ala Phe Cys Tyr Pro Cys Asn Pro Pro Pro Lys 280 285 290	17007
TGG TGA GCTCAGGGTC CCATTACCC CGCRAACCC CTCTGCGCGC CAGGGCGCGC Trp 295	17063
GCTCTATCTT TCTCTATGTC CCGTCGCCAC CGGCCTAAC GAACGGTGGC ACGGGGCCGC	17123
CCGGGAAAGC CTAGCTCCGC ACAGACACAG ACAGACAAAC GGCTCTCGA TTGCAACAAC	17183
GTGAAAAACA CACAATAATA TTACTTTATT TATTTTCGAC CGCTCGCGTG TCGCTCGTTT	17243
CTGGGGGGGG GGGGGGGTGT TGTTCGCTGT CCGCGGAGTG GGTGAGGGGG GAGAGTGGAC	17303

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GGAGGACAGT GTAAAAACCC GCGAGGTTGT CAGGGACGCG GAGGTAAGGA AGCCGCTAGA	17363
GGCGGTCATT CTCCTGCTCAA CGCGCGCCGCG CCAGCGCCAG CGCGATTCCA GCCTCCCTCG	17423
CAAAGATCGA GGCCTCACT TCGGGAGAGT TGGCGGCAGC CGCGCCGCGC CGCAAGGCGG	17483
CCAGGTATTG GCGACGGCGC ATCTCCGATT GCGGGACTCT CCCCGTCCC ACAGAGAAAA	17543
GACTCTGCAC GTAAATCGAG TCGTACAAAC ACGCTTCGCG GCACGGCCGA GGGTGCACAC	17603
AGCAGCACCA GTGCCCGGCC GCCAGGAGAG ACCGGGAGGT CTCTCGCTCG GCGACGCGA	17663
GGTCGGCCGG CAGGTGTCGG GACAGCCAGG ATAACAGTTC TTTCTCGATC ACGAAACGCA	17723
TATTCTCGCT CTGCATGGTA CGGCTCTCGT CCTCGAAGCG GTCACCGTCC AGAGAGTCGA	17783
GCCAGAAATC GCCCTCGATC CCTTCCATTG CCTCTCTAA TTCTCCCAAC CCGTTGCCGT	17843
TATTCGGGTC AGTGGGGGAG TTGGCGACGC TCTCCGTCGA CGCCACCGC GGCCTCAAAC	17903
CTAGGCCGCG CGTCGCCCGC CTGGCCCCCA GAAAAGCCGA ACGTAGCCGT TCGTTGGCAG	17963
CAATCAGCGC GTTCCGGCGG TCTCTCGCTG ACGTGAAGTC TCCGTAACCG TCCTTGAGTT	18023
CGGACGATAT CTCGACTAAC TCGCGCAGA GCCGCGAGGC GATCCGAATG CACGGGTCTA	18083
CCGAGTCGGC CGACTCCGAC GAGGCGACAG CGGCACCTTG CCGCTTCCGC TCGCCACGAG	18143
GTACCGCGTG CGCAGTAATG TGATCGTGT CCATCAGCGC CAGCGGGTAG CACCCGTCGA	18203
GCATGTTTTC CATTTAGGGA TGTGCTAGA GGAGAGCGGT CCGGGCGGTC TACTGCGGTT	18263
GTGCTGGGCC GAGTTGGACG GCTACGGATT GCGCCGGGCG TGAAGGGGGG GGGGCGGCGG	18323
GATGTCGGC GGTGCGAAAG GGGCGCGCGT CCGCTTCTGC GTGAAGGCTG AGCGGAAAG	18383
AAGTTCTGGA TGAGAAATGA TCGAGCGGGC AATAAATGTC CAGAGTAGGG GGGTGGGAGG	18443
GAGGGGGAGG TTCTGCCCGC CGTCTCTCTT ATCTGCTCGT CGAGGCTCTG GCCTTCGCTC	18503
GCCGTGCAGG GGTGAGGGCC GCTTCTCTT TTTTACTTCT CTCCTCGGAT TCCTGTCAG	18563
AGGAAGAAGA AAATGACAACT CTCCTCTTT TAAGAGTGCG CCTACCCGCC CTGGCGGCCG	18623
AAGCCTTCG TGGGTCTTTG CGGGCGCCG GAGAGCTGTC GTCAATAAAG TCTAAGTCAG ATTGCGTGGG	18683
AGCAAAATGGC GCGCGCGCCG GAGAGCTGTC GTCAATAAAG TCTAAGTCAG ATTGCGTGGG	18743
CTCTGACTCG GTGAGCTGT GTCCCGTGC CTCCTCGGCC AAGTCCACTC CCCGGCACCC	18803
AGGCTGCTCT TCCTCCGACT CCGGGTCTGCT CCAGCTCTCT CCGCGTGCCG GTTCTTCGTC	18863
CTCCGATACG TCCGAAAAGA AAAACTTCTG GGAGAGCTCT TCGGGATCC	18912

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Glu Asn Met Leu Asp Gly Cys Tyr Pro Leu Ala Leu Met Asp Ser
 1 5 10 15
 Asp His Ile Thr Ala His Ala Val Pro Arg Gly Glu Arg Arg Arg Gln
 20 25 30
 Gly Ala Ala Val Ala Ser Ser Glu Ser Ala Asp Ser Val Asp Pro Cys
 35 40 45
 Ile Arg Ile Ala Ser Arg Leu Trp Arg Glu Leu Val Glu Ile Ser Ser
 50 55 60
 Glu Leu Lys Asp Gly Tyr Gly Glu Phe Thr Ser Ala Arg Asp Arg Arg
 65 70 75 80
 Asn Ala Leu Ile Ala Ala Asn Glu Arg Leu Arg Ser Ala Phe Leu Gly
 85 90 95
 Ala Ser Arg Ala Thr Arg Gly Leu Gly Leu Arg Pro Arg Trp Ala Ser
 100 105 110
 Thr Glu Ser Val Ala Asn Ser Pro Thr Asp Pro Asn Asn Gly Asn Gly
 115 120 125
 Leu Gly Glu Leu Glu Glu Ala Met Glu Gly Ile Glu Gly Asp Phe Trp
 130 135 140
 Leu Asp Ser Leu Asp Gly Asp Arg Phe Glu Asp Glu Ser Arg Thr Met
 145 150 155 160
 Gln Ser Glu Asn Met Arg Phe Val Ile Glu Lys Glu Leu Leu Ser Trp
 165 170 175
 Leu Ser Arg His Leu Pro Ala Asp Leu Ala Ser Ala Glu Arg Glu Thr
 180 185 190
 Ser Arg Ser Leu Leu Ala Ala Gly His Trp Cys Cys Leu Trp His Pro
 195 200 205
 Arg Pro Cys Arg Glu Ala Cys Leu Tyr Asp Ser Ile Tyr Val Gln Ser
 210 215 220
 Leu Phe Cys Val Gly Thr Gly Arg Val Pro Gln Ser Glu Met Arg Arg
 225 230 235 240
 Arg Glu Tyr Leu Ala Ala Leu Arg Ala Gly Ala Ala Ala Asn Ser
 245 250 255
 Pro Glu Val Ser Ala Ser Ile Phe Ala Arg Asp Ala Gly Ile Ala Leu
 260 265 270
 Ala Leu Ala Arg Arg Arg
 275

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(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met Ser Lys Cys Tyr Cys Leu Ala Arg His Leu Tyr Lys Ser Pro Arg
1 5 10
Cys Val Gly Arg Arg Val Ala Phe Gly Gly Leu Ala Thr Met Ser Arg
20 25 30
Pro Pro Thr Ser His Leu Asp Leu Ala Phe Ser Ala Ala Phe Arg Gly
35 40 45
Thr Asp Leu Pro Gly Gly Arg Phe Trp Arg Ala Ser Gln Ser Cys Asp
50 55 60
Ile Phe Phe Trp Pro Asp Leu Ala Ala Val Ile Val Gln Ala Ala Arg
65 70 75 80
Ala Tyr Phe Glu Gly Lys Glu Arg Leu Gly Ser Leu Gln Val Ala Glu
85 90 95
Asp Ile Thr Ala His Asp Pro Arg Ile Ala Pro Ala Ala Lys Arg Ala
100 105 110
Val Ala Ala Ala Val Gly Leu Trp Thr Ala Leu Ser Glu Leu Val Gly
115 120 125
Gly Pro Asn Gly Glu Leu Glu Ser Lys Val Trp Gly Lys Gln Ile Pro
130 135 140
Arg Ala Ala Ala Trp Glu Ile Arg Asp Val Pro Lys Val Pro Val Ile
145 150 155 160
Gly Pro Asp Ile Leu Ser Phe Phe Ser Ala Ala Val Glu Leu Pro Val
165 170 175
Leu Tyr Ile Arg Ala Arg Gly Gly Ala His Ser Arg Ser Ala His Trp
180 185 190
Asn Asn Gln Ser Ser Ala Pro Ala Ala Gly Leu Ala Ala Ile Arg Ile
195 200 205
Gly Met Glu Met Val Arg Ser Leu Leu Val Ile Ala Leu Pro Leu Ser
210 215 220
Asn Phe Thr Leu Pro Glu Asp Leu Pro Glu Gly Ser Gln Asn Ser Ile
225 230 235 240
Arg Ala Phe Val Ala His Leu Met Asn Cys Val Ala Thr Asp Lys Ile
245 250 255
Met Ser Pro Asp Val Arg Val Pro Val Glu Glu Ser Phe Tyr Ser His
260 265 270
Cys Leu Arg Glu Ile Ile Met Cys Glu Arg Ala Phe Cys Tyr Pro Cys
275 280 285
Asn Pro Pro Pro Lys Trp
290

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(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Ala Pro Val Lys Val Thr Ile Val Ser Ala Val Asp Ser His Tyr
1 5 10 15
Lys Leu Pro Asn Ser Arg Phe Glu Leu Ser Asp Ser Gly Trp Lys Glu
20 25 30
Leu Val His Ala Val Lys Thr Met Ala Ser Tyr Asp Arg Pro Ser Thr
35 40 45
Leu Ser Val Ile Val Arg Pro Ala Ser Leu Tyr Glu Val Ser Gly Glu
50 55 60
Leu Phe Ser Leu Pro Arg Met Cys Arg Pro Val Ile Arg Phe Gly Glu
65 70 75 80
Gly Gly Asp Pro Pro Gly Val Ser Pro Glu Trp Ser Gly Leu Asp Ala
85 90 95
Gly Phe Tyr His Leu Ser Ser Gly Ala Tyr Ala Ala Lys Glu Phe His
100 105 110
Leu Trp Val Leu Gly Thr Ala Asp Ile Cys Met Ala Ala Leu Asn Leu
115 120 125
Pro Ala Pro Lys Thr Phe Leu Ile Thr Glu Thr Gly Gly Lys Asn Phe
130 135 140
Glu Arg Gly Val Glu Ile Phe Leu Val Asn Gly Asp Lys Thr Thr Leu
145 150 155 160
Ser Leu Ser His Pro Ser Val Trp Thr Thr Leu Ala Pro Ser Ser Leu
165 170 175
Arg Thr Pro Trp Pro Tyr Ser Thr Val Lys Phe Leu Lys Val Lys Pro
180 185 190
Asn Ser Ala Ala Tyr Cys Val Ser Asp Ser Asp Gly Glu Arg Gln
195 200 205
Pro Lys Phe Phe Leu Gly Ser Leu Phe Lys Ser Lys Lys Pro Arg Ser
210 215 220
Pro Arg Arg Arg
225

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Arg Phe Arg Arg Ile Cys Ser Arg Ser Arg Ala Glu Lys Arg Arg
1 5 10 15
Arg Thr Thr Glu Asn Pro Leu Thr Ser Lys Arg Val Cys Val Leu Asp
20 25 30
Ser Phe Ser Arg Thr Met Ser Leu Arg Pro Tyr Ala Glu Ile Leu Pro
35 40 45

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Thr Ala Glu Gly Val Glu Arg Leu Ala Glu Leu Val Ser Val Thr Met
50 55 60

Thr Glu Arg Ala Glu Pro Val Thr Glu Asn Thr Ala Val Asn Ser Ile
65 70 75 80

Pro Pro Ala Asn Glu Asn Gly Gln Asn Phe Ala Tyr Ala Gly Asp Gly
85 90 95

Pro Ser Thr Thr Glu Lys Val Asp Gly Ser His Thr Asp Phe Asp Glu
100 105 110

Ala Ser Ser Asp Tyr Ala Gly Pro Val Pro Leu Ala Gln Thr Arg Leu
115 120 125

Lys His Ser Asp Glu Phe Leu Gln His Phe Arg Val Leu Asp Asp Leu
130 135 140

Val Glu Gly Ala Tyr Gly Phe Ile Cys Asp Val Arg Arg Tyr Thr Glu
145 150 155 160

Glu Glu Gln Arg Arg Arg Gly Val Asn Ser Thr Asn Gln Gly Lys Ser
165 170 175

Lys Cys Lys Arg Leu Ile Ala Lys Tyr Val Lys Asn Gly Thr Arg Ala
180 185 190

Ala Ser Gln Leu Glu Asn Glu Ile Leu Val Leu Gly Arg Leu Asn His
195 200 205

Glu Asn Val Leu Lys Ile Gln Glu Ile Leu Arg Tyr Pro Asp Asn Thr
210 215 220

Tyr Met Leu Thr Gln Arg Tyr Gln Phe Asp Leu Tyr Ser Tyr Met Tyr
225 230 235 240

Asp Glu Ala Phe Asp Trp Lys Asp Ser Pro Met Leu Lys Gln Thr Arg
245 250 255

Arg Ile Met Lys Gln Leu Met Ser Ala Val Ser Tyr Ile His Ser Lys
260 265 270

Lys Leu Ile His Arg Asp Ile Lys Leu Glu Asn Ile Phe Leu Asn Cys
275 280 285

Asp Gly Lys Thr Val Leu Gly Asp Phe Gly Thr Val Thr Pro Phe Glu
290 295 300

Asn Glu Arg Glu Pro Phe Glu Tyr Gly Trp Val Gly Thr Val Ala Thr
305 310 315 320

Asn Ser Pro Glu Ile Leu Ala Arg Asp Ser Tyr Cys Glu Ile Thr Asp
325 330 335

Ile Trp Ser Cys Gly Val Val Leu Leu Glu Met Val Ser His Glu Phe
340 345 350

Cys Pro Ile Gly Asp Gly Gly Gly Asn Pro His Gln Leu Leu Lys
355 360 365

Val Ile Asp Ser Leu Ser Val Cys Asp Glu Glu Phe Pro Asp Pro Pro
370 375 380

Cys Asn Leu Tyr Asn Tyr Leu His Tyr Ala Ser Ile Asp Arg Ala Gly
385 390 395 400

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His Thr Val Pro Ser Leu Ile Arg Asn Leu His Leu Pro Ala Asp Val
 405 410 415
 Glu Tyr Pro Leu Val Lys Met Leu Thr Phe Asp Trp Arg Leu Arg Pro
 420 425 430
 Ser Ala Ala Glu Val Leu Ala Met Pro Leu Phe Ser Ala Glu Glu Glu
 435 440 445
 Arg Thr Ile Thr Ile Ile His Gly Lys His Lys Pro Ile Arg Pro Glu
 450 455 460
 Ile Arg Ala Arg Val Pro Arg Ser Met Ser Glu Gly
 465 470 475

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Thr Leu Pro His Arg Leu Thr Lys Arg Pro Phe Ala Arg Arg Phe
 1 5 10 15
 Cys Ser Val Phe Val Ile His Tyr Ser Glu Thr Lys Leu Asp Arg Tyr
 20 25 30
 Asn Lys Thr Met Leu Leu Tyr Arg Pro Asp Ser Thr Met Arg His Ser
 35 40 45
 Gly Gly Asp Ala Asn His Arg Gly Ile Arg Pro Arg Arg Lys Ser Ile
 50 55 60
 Gly Ala Phe Ser Ala Arg Glu Lys Thr Gly Lys Arg Asn Ala Leu Thr
 65 70 75 80
 Glu Ser Ser Ser Ser Ser Asp Met Leu Asp Pro Phe Ser Thr Asp Lys
 85 90 95
 Glu Phe Gly Gly Lys Trp Thr Val Asp Gly Pro Ala Asp Ile Thr Ala
 100 105 110
 Glu Val Leu Ser Gln Ala Trp Asp Val Leu Gln Leu Val Lys His Glu
 115 120 125
 Asp Ala Glu Glu Glu Arg Val Thr Tyr Glu Ser Lys Pro Thr Pro Ile
 130 135 140
 Gln Pro Phe Asn Ala Trp Pro Asp Gly Pro Ser Trp Asn Ala Gln Asp
 145 150 155 160
 Phe Thr Arg Ala Pro Ile Val Tyr Pro Ser Ala Glu Val Leu Asp Ala
 165 170 175
 Glu Ala Leu Lys Val Gly Ala Phe Val Ser Arg Val Leu Gln Cys Val
 180 185 190
 Pro Phe Thr Arg Ser Lys Lys Ser Val Thr Val Arg Asp Ala Gln Ser
 195 200 205

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Phe Leu Gly Asp Ser Phe Trp Arg Ile Met Gln Asn Val Tyr Thr Val
 210 215 220
 Val Leu Arg Gln His Ile Thr Arg Leu Arg His Pro Ser Ser Lys Ser
 225 230 235 240
 Ile Val Asn Cys Asn Asp Pro Leu Trp Tyr Ala Tyr Ala Asn Gln Phe
 245 250 255
 His Trp Arg Gly Met Arg Val Pro Ser Leu Lys Leu Ala Ser Pro Pro
 260 265 270
 Glu Glu Asn Ile Gln His Gly Pro Met Ala Ala Val Phe Arg Asn Ala
 275 280 285
 Gly Ala Gly Leu Phe Leu Trp Pro Ala Met Arg Ala Phe Glu Glu
 290 295 300
 Arg Asp Lys Arg Leu Leu Arg Ala Cys Leu Ser Ser Leu Asp Ile Met
 305 310 315 320
 Asp Ala Ala Val Leu Ala Ser Phe Pro Phe Tyr Trp Arg Gly Val Gln
 325 330 335
 Asp Thr Ser Arg Phe Glu Pro Ala Leu Gly Cys Leu Ser Glu Tyr Phe
 340 345 350
 Ala Leu Val Val Leu Leu Ala Glu Thr Val Leu Ala Thr Met Phe Asp
 355 360 365
 His Ala Leu Val Phe Met Arg Ala Leu Ala Asp Gly Asn Phe Asp Asp
 370 375 380
 Tyr Asp Glu Thr Arg Tyr Ile Asp Pro Val Lys Asn Glu Tyr Leu Asn
 385 390 395 400
 Gly Ala Glu Gly Thr Leu Leu Arg Gly Ile Val Ala Ser Asn Thr Ala
 405 410 415
 Leu Ala Val Val Cys Ala Asn Thr Tyr Ser Thr Ile Arg Lys Leu Pro
 420 425 430
 Ser Val Ala Thr Ser Ala Cys Asn Val Ala Tyr Arg Thr Glu Thr Leu
 435 440 445
 Lys Ala Arg Arg Pro Gly Met Ser Asp Ile Tyr Arg Ile Leu Gln Lys
 450 455 460
 Glu Phe Phe Phe Tyr Ile Ala Trp Leu Gln Arg Val Ala Thr His Ala
 465 470 475 480
 Asn Phe Cys Leu Asn Ile Leu Lys Arg Ser Val Asp Thr Gly Ala Pro
 485 490 495
 Pro Phe Leu Phe Arg Ala Ser Ser Glu Lys Arg Leu Gln Gln Leu Asn
 500 505 510
 Lys Met Leu Cys Pro Leu Leu Val Pro Ile Gln Tyr Glu Asp Phe Ser
 515 520 525
 Lys Ala Met Gly Ser Glu Leu Lys Arg Glu Lys Leu Glu Thr Phe Val
 530 535 540
 Lys Ala Ile Ser Ser Asp Arg Asp Pro Arg Gly Ser Leu Arg Phe Leu
 545 550 555 560

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Ile Ser Asp His Ala Arg Glu Ile Ile Ala Asp Gly Val Arg Phe Lys
 565 570 575
 Pro Val Ile Asp Glu Pro Val Arg Ala Ser Val Ala Leu Ser Thr Ala
 580 585 590
 Ala Ala Gly Lys Val Lys Ala Arg Leu Thr Ser Val Arg Ala Pro
 595 600 605
 Val Pro Gly Ala Gly Ala Val Ser Ala Arg Arg Lys Ser Glu Ile
 610 615 620

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Ser Gly Phe Ser Asn Ile Gly Ser Ile Ala Thr Val Ser Leu Val
 1 5 10 15
 Cys Ser Leu Leu Cys Ala Ser Val Leu Gly Ala Pro Val Leu Asp Gly
 20 25 30
 Leu Glu Ser Ser Pro Phe Pro Phe Gly Gly Lys Ile Ile Ala Gln Ala
 35 40 45
 Cys Asn Arg Thr Thr Ile Glu Val Thr Val Pro Trp Ser Asp Tyr Ser
 50 55 60
 Gly Arg Thr Glu Gly Val Ser Val Glu Val Lys Trp Phe Tyr Gly Asn
 65 70 75 80
 Ser Asn Pro Glu Ser Phe Val Phe Gly Val Asp Ser Glu Thr Gly Ser
 85 90 95
 Gly His Glu Asp Leu Ser Thr Cys Trp Ala Leu Ile His Asn Leu Asn
 100 105 110
 Ala Ser Val Cys Arg Ala Ser Asp Ala Gly Ile Pro Asp Phe Asp Lys
 115 120 125
 Gln Cys Glu Lys Val Gln Arg Arg Leu Arg Ser Gly Val Glu Leu Gly
 130 135 140
 Ser Tyr Val Ser Gly Asn Gly Ser Leu Val Leu Tyr Pro Gly Met Tyr
 145 150 155 160
 Asp Ala Gly Ile Tyr Ala Tyr Gln Leu Ser Val Gly Gly Lys Gly Tyr
 165 170 175
 Thr Gly Ser Val Tyr Leu Asp Val Gly Pro Asn Pro Gly Cys His Asp
 180 185 190
 Gln Tyr Gly Tyr Thr Tyr Tyr Ser Leu Ala Asp Glu Ala Ser Asp Leu
 195 200 205
 Ser Ser Tyr Asp Val Ala Ser Pro Glu Leu Asp Gly Pro Met Glu Glu
 210 215 220

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Asp Tyr Ser Asn Cys Leu Asp Met Pro Pro Leu Arg Pro Trp Thr Thr 240
225 230 235
Val Cys Ser His Asp Val Glu Glu Gln Glu Asn Ala Thr Asp Glu Leu 255
245 250
Tyr Leu Trp Asp Glu Glu Cys Ala Gly Pro Leu Asp Glu Tyr Val Asp 270
260 265
Glu Arg Ser Glu Thr Met Pro Arg Met Val Val Phe Ser Pro Pro Ser 285
275 280
Thr Leu Gln Gln 290

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 985 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Gly Thr Met Leu Val Leu Arg Leu Phe Leu Leu Ala Val Ala Asp 15
1 5 10
Ala Ala Leu Pro Thr Gly Arg Phe Cys Arg Val Trp Lys Val Pro Pro 30
20 25 30
Gly Gly Thr Ile Gln Glu Asn Leu Ala Val Leu Ala Glu Ser Pro Val 45
35 40 45
Thr Gly His Ala Thr Tyr Pro Pro Pro Glu Gly Ala Val Ser Phe Gln 60
50 55 60
Ile Phe Ala Asp Thr Pro Thr Leu Arg Ile Arg Tyr Gly Ala Thr Glu 80
65 70 75 80
Asp Glu Leu Ala Leu Glu Arg Gly Thr Ser Ala Ser Asp Ala Asp Asn 95
85 90 95
Val Thr Phe Ser Leu Ser Tyr Arg Pro Arg Pro Glu Ile His Gly Ala 110
100 105 110
Tyr Phe Thr Ile Gly Val Phe Ala Thr Gly Gln Ser Thr Glu Ser Ser 125
115 120 125
Tyr Ser Val Ile Ser Arg Val Leu Val Asn Ala Ser Leu Glu Arg Ser 140
130 135 140
Val Arg Leu Glu Thr Pro Cys Asp Glu Asn Phe Leu Gln Asn Glu Pro 160
145 150 155 160
Thr Trp Gly Ser Lys Arg Trp Leu Gly Pro Pro Ser Pro Tyr Val Arg 175
165 170 175
Asp Asn Asp Val Ala Val Leu Thr Lys Ala Gln Tyr Ile Gly Glu Cys 190
180 185 190
Tyr Ser Asn Ser Ala Ala Gln Thr Gly Leu Thr Ser Leu Asn Met Thr 205
195 200 205

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Phe Phe Tyr Ser Pro Lys Arg Ile Val Asn Val Thr Trp Thr Thr Gly
 210 215 220
 Gly Pro Ser Pro Ser Arg Ile Thr Val Tyr Ser Ser Arg Glu Asn Gly
 225 230 235 240
 Gln Pro Val Leu Arg Asn Val Ser Asp Gly Phe Leu Val Lys Tyr Thr
 245 250 255
 Pro Asp Ile Asp Gly Arg Ala Met Ile Asn Val Ile Ala Asn Tyr Ser
 260 265 270
 Pro Ala Asp Ser Gly Ser Val Leu Ala Phe Thr Ala Phe Arg Glu Gly
 275 280 285
 Lys Leu Pro Ser Ala Ile Gln Leu His Arg Ile Asp Met Ser Gly Thr
 290 295 300
 Glu Pro Pro Gly Thr Glu Thr Thr Phe Asp Cys Gln Lys Met Ile Glu
 305 310 315 320
 Thr Pro Tyr Arg Ala Leu Gly Ser Asn Val Pro Arg Asp Asp Ser Ile
 325 330 335
 Arg Pro Gly Ala Thr Leu Pro Pro Phe Asp Thr Ala Ala Pro Asp Phe
 340 345 350
 Asp Thr Gly Thr Ser Pro Thr Pro Thr Thr Val Pro Glu Pro Ala Ile
 355 360 365
 Thr Thr Leu Ile Pro Arg Ser Thr Ser Asp Met Gly Phe Phe Ser Thr
 370 375 380
 Ala Arg Ala Thr Gly Ser Glu Thr Leu Ser Val Pro Val Gln Glu Thr
 385 390 395 400
 Asp Arg Thr Leu Ser Thr Thr Pro Leu Thr Leu Pro Leu Thr Pro Gly
 405 410 415
 Glu Ser Glu Asn Thr Leu Phe Pro Thr Thr Ala Pro Gly Ile Ser Thr
 420 425 430
 Glu Thr Pro Ser Ala Ala His Glu Thr Thr Gln Thr Gln Ser Ala Glu
 435 440 445
 Thr Val Val Phe Thr Gln Ser Pro Ser Thr Glu Ser Glu Thr Ala Arg
 450 455 460
 Ser Gln Ser Gln Glu Pro Trp Tyr Phe Thr Gln Thr Pro Ser Thr Glu
 465 470 475 480
 Gln Ala Ala Leu Thr Gln Thr Gln Ile Ala Glu Thr Glu Ala Leu Phe
 485 490 495
 Thr Gln Thr Pro Ser Ala Glu Gln Met Thr Phe Thr Gln Thr Pro Gly
 500 505 510
 Ala Glu Thr Glu Ala Pro Ala Gln Thr Pro Ser Thr Ile Pro Glu Ile
 515 520 525
 Phe Thr Gln Ser Arg Ser Thr Pro Pro Glu Thr Ala Arg Ala Pro Ser
 530 535 540
 Ala Ala Pro Glu Val Phe Thr Gln Ser Ser Ser Thr Val Thr Glu Val
 545 550 555 560

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Phe Thr Gln Thr Pro Ser Thr Val Pro Lys Thr Thr Leu Ser Ser Ser
 565 570 575
 Thr Glu Pro Ala Ile Phe Thr Arg Thr Gln Ser Ala Gly Thr Glu Ala
 580 585 590
 Phe Thr Gln Thr Ser Ser Ala Glu Pro Asp Thr Met Arg Thr Gln Ser
 595 600 605
 Thr Glu Thr His Phe Phe Thr Gln Ala Pro Ser Thr Val Pro Lys Ala
 610 615 620
 Thr Gln Thr Pro Ser Thr Glu Pro Glu Val Leu Thr Gln Ser Pro Ser
 625 630 635 640
 Thr Glu Pro Val Pro Phe Thr Arg Thr Leu Gly Ala Glu Pro Glu Ile
 645 650 655
 Thr Gln Thr Pro Ser Ala Ala Pro Glu Val Tyr Thr Arg Ser Ser Ser
 660 665 670
 Thr Met Pro Glu Thr Ala Gln Ser Thr Pro Leu Ala Ser Gln Asn Pro
 675 680 685
 Thr Ser Ser Gly Thr Gly Thr His Asn Thr Glu Pro Arg Thr Tyr Pro
 690 695 700
 Val Gln Thr Thr Pro His Thr Gln Lys Leu Tyr Thr Glu Asn Lys Thr
 705 710 715 720
 Leu Ser Phe Pro Thr Val Val Ser Glu Phe His Glu Met Ser Thr Ala
 725 730 735
 Glu Ser Gln Thr Pro Leu Leu Asp Val Lys Ile Val Glu Val Lys Phe
 740 745 750
 Ser Asn Asp Gly Glu Val Thr Ala Thr Cys Val Ser Thr Val Lys Ser
 755 760 765
 Pro Tyr Arg Val Glu Thr Asn Trp Lys Val Asp Leu Val Asp Val Met
 770 775 780
 Asp Glu Ile Ser Gly Asn Ser Pro Ala Gly Val Phe Asn Ser Asn Glu
 785 790 795 800
 Lys Trp Gln Lys Gln Leu Tyr Tyr Arg Val Thr Asp Gly Arg Thr Ser
 805 810 815
 Val Gln Leu Met Cys Leu Ser Cys Thr Ser His Ser Pro Glu Pro Tyr
 820 825 830
 Cys Leu Phe Asp Thr Ser Leu Ile Ala Arg Glu Lys Asp Ile Ala Pro
 835 840 845
 Glu Leu Tyr Phe Thr Ser Asp Pro Gln Thr Ala Tyr Cys Thr Ile Thr
 850 855 860
 Leu Pro Ser Gly Val Val Pro Arg Phe Glu Trp Ser Leu Asn Asn Val
 865 870 875 880
 Ser Leu Pro Glu Tyr Leu Thr Ala Thr Thr Val Val Ser His Thr Ala
 885 890 895
 Gly Gln Ser Thr Val Trp Lys Ser Ser Ala Arg Ala Gly Glu Ala Trp
 900 905 910

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Ile Ser Gly Arg Gly Gly Asn Ile Tyr Glu Cys Thr Val Leu Ile Ser
 915 920 925
 Asp Gly Thr Arg Val Thr Thr Arg Lys Glu Arg Cys Leu Thr Asn Thr
 930 935 940
 Trp Ile Ala Val Glu Asn Gly Ala Ala Gln Ala Gln Leu Tyr Ser Leu
 945 950 955 960
 Phe Ser Gly Leu Val Ser Gly Leu Cys Gly Ser Ile Ser Ala Leu Tyr
 965 970 975
 Ala Thr Leu Trp Thr Ala Ile Tyr Phe
 980 985

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 434 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met His Arg Pro His Leu Arg Arg His Ser Arg Tyr Tyr Ala Lys Gly
 1 5 10 15
 Glu Val Leu Asn Lys His Met Asp Cys Gly Gly Lys Arg Cys Cys Ser
 20 25 30
 Gly Ala Ala Val Phe Thr Leu Phe Trp Thr Cys Val Arg Ile Met Arg
 35 40 45
 Glu His Ile Cys Phe Val Arg Asn Ala Met Asp Arg His Leu Phe Leu
 50 55 60
 Arg Asn Ala Phe Trp Thr Ile Val Leu Leu Ser Ser Phe Ala Ser Gln
 65 70 75 80
 Ser Thr Ala Ala Val Thr Tyr Asp Tyr Ile Leu Gly Arg Arg Ala Leu
 85 90 95
 Asp Ala Leu Thr Ile Pro Ala Val Gly Pro Tyr Asn Arg Tyr Leu Thr
 100 105 110
 Arg Val Ser Arg Gly Cys Asp Val Val Glu Leu Asn Pro Ile Ser Asn
 115 120 125
 Val Asp Asp Met Ile Ser Ala Ala Lys Glu Lys Glu Lys Gly Gly Pro
 130 135 140
 Phe Glu Ala Ser Val Val Trp Phe Tyr Val Ile Lys Gly Asp Asp Gly
 145 150 155 160
 Glu Asp Lys Tyr Cys Pro Ile Tyr Arg Lys Glu Tyr Arg Glu Cys Gly
 165 170 175
 Asp Val Gln Leu Leu Ser Glu Cys Ala Val Gln Ser Ala Gln Met Trp
 180 185 190
 Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly
 195 200 205

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Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu
 210 215 220
 Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu
 225 230 235 240
 Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro
 245 250 255
 Ser Lys Cys Trp Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu
 260 265 270
 His Leu Tyr Pro Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val
 275 280 285
 Tyr Arg Gly Tyr Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg
 290 295 300
 Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln
 305 310 315 320
 Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala
 325 330 335
 Glu Ser Ser Glu Lys Lys Ala Pro Glu Asp Ser Glu Asp Asp Met
 340 345 350
 Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp
 355 360 365
 Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp
 370 375 380
 Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys
 385 390 395 400
 Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys
 405 410 415
 Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala
 420 425 430
 Arg Ser .

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Ala Ser Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr Leu Ala
 1 5 10 15
 Pro Phe Gly Ala Met Gly Ile Val Ile Thr Gly Asn His Val Ser Ala
 20 25 30
 Arg Ile Asp Asp Asp His Ile Val Ile Val Ala Pro Arg Pro Glu Ala
 35 40 45

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Thr Ile Gln Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro His Lys
50 55 60

Pro Tyr Ser Gly Thr Val Arg Val Ala Phe Arg Ser Asp Ile Thr Asn
65 70 75 80

Gln Cys Tyr Gln Glu Leu Ser Glu Glu Arg Phe Glu Asn Cys Thr His
85 90 95

Arg Ser Ser Ser Val Phe Val Gly Cys Lys Val Thr Glu Tyr Thr Phe
100 105 110

Ser Ala Ser Asn Arg Leu Thr Gly Pro Pro His Pro Phe Lys Leu Thr
115 120 125

Ile Arg Asn Pro Arg Pro Asn Asp Ser Gly Met Phe Tyr Val Ile Val
130 135 140

Arg Leu Asp Asp Thr Lys Glu Pro Ile Asp Val Phe Ala Ile Gln Leu
145 150 155 160

Ser Val Tyr Gln Phe Ala Asn Thr Ala Thr Arg Gly Leu Tyr Ser
165 170 175

Lys Ala Ser Cys Arg Thr Phe Gly Leu Pro Thr Val Gln Leu Glu Ala
180 185 190

Tyr Leu Arg Thr Glu Glu Ser Trp Arg Asn Trp Gln Ala Tyr Val Ala
195 200 205

Thr Glu Ala Thr Thr Thr Ser Ala Glu Ala Thr Thr Pro Thr Pro Val
210 215 220

Thr Ala Thr Ser Ala Ser Glu Leu Glu Ala Glu His Phe Thr Phe Pro
225 230 235 240

Trp Leu Glu Asn Gly Val Asp His Tyr Glu Pro Thr Pro Ala Asn Glu
245 250 255

Asn Ser Asn Val Thr Val Arg Leu Gly Thr Met Ser Pro Thr Leu Ile
260 265 270

Gly Val Thr Val Ala Ala Val Val Ser Ala Thr Ile Gly Leu Val Ile
275 280 285

Val Ile Ser Ile Val Thr Arg Asn Met Cys Thr Pro His Arg Lys Leu
290 295 300

Asp Thr Val Ser Gln Asp Asp Glu Glu Arg Ser Gln Thr Arg Arg Glu
305 310 315 320

Ser Arg Lys Phe Gly Pro Met Val Ala Cys Glu Ile Asn Lys Gly Ala
325 330 335

Asp Gln Asp Ser Glu Leu Val Glu Leu Val Ala Ile Val Asn Pro Ser
340 345 350

Ala Leu Ser Ser Pro Asp Ser Ile Lys Met
355 360

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(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Asn Met Leu Val Ile Val Leu Ala Ser Cys Leu Ala Arg Leu Thr
1 5 10 15
Phe Ala Thr Arg His Val Leu Phe Leu Glu Gly Thr Gln Ala Val Leu
20 25 30
Gly Glu Asp Asp Pro Arg Asn Val Pro Glu Gly Thr Val Ile Lys Trp
35 40 45
Thr Lys Val Leu Arg Asn Ala Cys Lys Met Lys Ala Ala Asp Val Cys
50 55 60
Ser Ser Pro Asn Tyr Cys Phe His Asp Leu Ile Tyr Asp Gly Gly Lys
65 70 75 80
Lys Asp Cys Pro Pro Ala Gly Pro Leu Ser Ala Asn Leu Val Ile Leu
85 90 95
Leu Lys Arg Gly Glu Ser Phe Val Val Leu Gly Ser Gly Leu His Asn
100 105 110
Ser Asn Ile Thr Asn Ile Met Trp Thr Glu Tyr Gly Gly Leu Leu Phe
115 120 125
Asp Pro Val Thr Arg Ser Asp Glu Gly Ile Tyr Phe Arg Arg Ile Ser
130 135 140
Gln Pro Asp Leu Ala Met Glu Thr Thr Ser Tyr Asn Val Ser Val Leu
145 150 155 160
Ser His Val Asp Glu Lys Ala Pro Ala Pro His Glu Val Glu Ile Asp
165 170 175
Thr Ile Lys Pro Ser Glu Ala His Ala His Val Glu Leu Gln Met Leu
180 185 190
Pro Phe His Glu Leu Asn Asp Asn Ser Pro Thr Tyr Val Thr Pro Val
195 200 205
Leu Arg Val Phe Pro Pro Thr Glu His Val Lys Phe Asn Val Thr Tyr
210 215 220
Ser Trp Tyr Gly Phe Asp Val Lys Glu Glu Cys Glu Glu Val Lys Leu
225 230 235 240
Phe Glu Pro Cys Val Tyr His Pro Thr Asp Gly Lys Cys Gln Phe Pro
245 250 255
Ala Thr Asn Gln Arg Cys Leu Ile Gly Ser Val Leu Met Ala Glu Phe
260 265 270
Leu Gly Ala Ala Ser Leu Leu Asp Cys Ser Arg Asp Thr Leu Glu Asp
275 280 285
Cys His Glu Asn Arg Val Pro Asn Leu Arg Phe Asp Ser Arg Leu Ser
290 295 300
Glu Ser Arg Ala Gly Leu Val Ile Ser Pro Leu Ile Ala Ile Pro Lys
305 310 315 320
Val Leu Ile Ile Val Val Ser Asp Gly Asp Ile Leu Gly Trp Ser Tyr
325 330 335

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Thr Val Leu Gly Lys Arg Asn Ser Pro Arg Val Val Val Glu Thr His
340 345 350
Met Pro Ser Lys Val Pro Met Asn Lys Val Val Ile Gly Ser Pro Gly
355 360 365
Pro Met Asp Glu Thr Gly Asn Tyr Lys Met Tyr Phe Val Val Ala Gly
370 375 380
Val Ala Ala Thr Cys Val Ile Leu Thr Cys Ala Leu Leu Val Gly Lys
385 390 395 400
Lys Lys Cys Pro Ala His Gln Met Gly Thr Phe Ser Lys Thr Glu Pro
405 410 415
Leu Tyr Ala Pro Leu Pro Lys Asn Glu Phe Glu Ala Gly Gly Leu Thr
420 425 430
Asp Asp Glu Glu Val Ile Tyr Asp Glu Val Tyr Glu Pro Leu Phe Arg
435 440 445
Gly Tyr Cys Lys Gln Glu Phe Arg Glu Asp Val Asn Thr Phe Phe Gly
450 455 460
Ala Val Val Glu Gly Glu Arg Ala Leu Asn Phe Lys Ser Ala Ile Ala
465 470 475 480
Ser Met Ala Asp Arg Ile Leu Ala Asn Lys Ser Gly Arg Arg Asn Met
485 490 495
Asp Ser Tyr .

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Pro Phe Lys Thr Arg Gly Ala Glu Asp Ala Ala Ala Gly Lys Asn
1 5 10 15
Arg Phe Lys Lys Ser Arg Asn Arg Glu Ile Leu Pro Thr Arg Leu Arg
20 25 30
Gly Thr Gly Lys Lys Thr Ala Gly Leu Ser Asn Tyr Thr Gln Pro Ile
35 40 45
Pro Trp Asn Pro Lys Phe Cys Ser Ala Arg Gly Glu Ser Asp Asn His
50 55 60
Ala Cys Lys Asp Thr Phe Tyr Arg Arg Thr Cys Cys Ala Ser Arg Ser
65 70 75 80
Thr Val Ser Ser Gln Pro Asp Ser Pro His Thr Pro Met Pro Thr Glu
85 90 95
Tyr Gly Arg Val Pro Ser Ala Lys Arg Lys Lys Leu Ser Ser Ser Asp
100 105 110

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Cys Glu Gly Ala His Gln Pro Leu Val Ser Cys Lys Leu Pro Asp Ser
 115 120 125
 Gln Ala Ala Pro Ala Arg Thr Tyr Ser Ser Ala Gln Arg Tyr Thr Val
 130 135 140
 Asp Glu Val Ser Ser Pro Thr Pro Pro Gly Val Asp Ala Val Ala Asp
 145 150 155 160
 Leu Glu Thr Arg Ala Glu Leu Pro Gly Ala Thr Thr Glu Gln Thr Glu
 165 170 175
 Ser Lys Asn Lys Leu Pro Asn Gln Gln Ser Arg Leu Lys Pro Lys Pro
 180 185 190
 Thr Asn Glu His Val Gly Gly Glu Arg Cys Pro Ser Glu Gly Thr Val
 195 200 205
 Glu Ala Pro Ser Leu Gly Ile Leu Ser Arg Val Gly Ala Ala Ile Ala
 210 215 220
 Asn Glu Leu Ala Arg Met Arg Arg Ala Cys Leu Pro Leu Ala Ala Ser
 225 230 235 240
 Ala Ala Ala Ala Gly Ile Val Ala Trp Ala Ala Ala Arg Ala Leu Gln
 245 250 255
 Lys Gln Gly Arg
 260

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Ser Lys Cys Tyr Cys Leu Ala Arg His Leu Tyr Lys Ser Pro Arg
 1 5 10 15
 Cys Val Gly Arg Arg Val Ala Phe Gly Gly Leu Ala Thr Met Ser Arg
 20 25 30
 Pro Pro Thr Ser His Leu Asp Leu Ala Phe Ser Ala Ala Phe Arg Gly
 35 40 45
 Thr Asp Leu Pro Gly Gly Arg Phe Trp Arg Ala Ser Gln Ser Cys Asp
 50 55 60
 Ile Phe Phe Trp Pro Asp Leu Ala Ala Val Ile Val Gln Ala Ala Arg
 65 70 75 80
 Ala Tyr Phe Glu Gly Lys Glu Arg Leu Gly Ser Leu Gln Val Ala Glu
 85 90 95
 Asp Ile Thr Ala His Asp Pro Arg Ile Ala Pro Ala Ala Lys Arg Ala
 100 105 110
 Val Ala Ala Ala Val Gly Leu Trp Thr Ala Leu Ser Glu Leu Val Gly
 115 120 125

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Gly Pro Asn Gly Glu Leu Glu Ser Lys Val Trp Gly Lys Gln Ile Pro
 130 135 140
 Arg Ala Ala Ala Trp Glu Ile Arg Asp Val Pro Lys Val Pro Val Ile
 145 150 155 160
 Gly Pro Asp Ile Leu Ser Phe Phe Ser Ala Ala Val Glu Leu Pro Val
 165 170 175
 Leu Tyr Ile Arg Ala Arg Gly Gly Ala His Ser Arg Ser Ala His Trp
 180 185 190
 Asn Asn Gln Ser Ser Ala Pro Ala Ala Gly Leu Ala Ala Ile Arg Ile
 195 200 205
 Gly Met Glu Met Val Arg Ser Leu Leu Val Ile Ala Leu Pro Leu Ser
 210 215 220
 Asn Phe Thr Leu Pro Glu Asp Leu Pro Glu Gly Ser Gln Asn Ser Ile
 225 230 235 240
 Arg Ala Phe Val Ala His Leu Met Asn Cys Val Ala Thr Asp Lys Ile
 245 250 255
 Met Ser Pro Asp Val Arg Val Pro Val Glu Glu Ser Phe Tyr Ser His
 260 265 270
 Cys Leu Arg Glu Ile Ile Met Cys Glu Arg Ala Phe Cys Tyr Pro Cys
 275 280 285
 Asn Pro Pro Pro Lys Trp
 290

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Glu Asn Met Leu Asp Gly Cys Tyr Pro Leu Ala Leu Met Asp Ser
 1 5 10 15
 Asp His Ile Thr Ala His Ala Val Pro Arg Gly Glu Arg Arg Gln
 20 25 30
 Gly Ala Ala Val Ala Ser Ser Glu Ser Ala Asp Ser Val Asp Pro Cys
 35 40 45
 Ile Arg Ile Ala Ser Arg Leu Trp Arg Glu Leu Val Glu Ile Ser Ser
 50 55 60
 Glu Leu Lys Asp Gly Tyr Gly Glu Phe Thr Ser Ala Arg Asp Arg Arg
 65 70 75 80
 Asn Ala Leu Ile Ala Ala Asn Glu Arg Leu Ser Ala Phe Leu Gly
 85 90 95
 Ala Ser Arg Ala Thr Arg Gly Leu Gly Leu Arg Pro Arg Trp Ala Ser
 100 105 110

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Thr Glu Ser Val Ala Asn Ser Pro Thr Asp Pro Asn Asn Gly Asn Gly
 115 120 125
 Leu Gly Glu Leu Glu Glu Ala Met Glu Gly Ile Glu Gly Asp Phe Trp
 130 135 140
 Leu Asp Ser Leu Asp Gly Asp Arg Phe Glu Asp Glu Ser Arg Thr Met
 145 150 155 160
 Gln Ser Glu Asn Met Arg Phe Val Ile Glu Lys Glu Leu Leu Ser Trp
 165 170 175
 Leu Ser Arg His Leu Pro Ala Asp Leu Ala Ser Ala Glu Arg Glu Thr
 180 185 190
 Ser Arg Ser Leu Leu Ala Ala Gly His Trp Cys Cys Leu Trp His Pro
 195 200 205
 Arg Pro Cys Arg Glu Ala Cys Leu Tyr Asp Ser Ile Tyr Val Gln Ser
 210 215 220
 Leu Phe Cys Val Gly Thr Gly Arg Val Pro Gln Ser Glu Met Arg Arg
 225 230 235 240
 Arg Glu Tyr Leu Ala Ala Leu Arg Ala Gly Ala Ala Ala Asn Ser
 245 250 255
 Pro Glu Val Ser Ala Ser Ile Phe Ala Arg Asp Ala Gly Ile Ala Leu
 260 265 270
 Ala Leu Ala Arg Arg Arg .
 275

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